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MPSRCH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 18 13:58:30 2000; MasPar time 58.81 Seconds
339.279 Million cell updates/sec
Tabular output not generated.

Title: >US-09-490-187-2
Description: (1-423) from US09490187.pep
Perfect Score: 3111
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....AVIHPATQTSLQVRQRLGSL 423

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir62
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 46.931; Variance 84.207; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	170	5.5	272	2	I48700	gene ox40 protein - m	2.81e-12
2	149	4.8	271	2	S12783	OX40 antigen precurso	1.30e-08
3	146	4.7	416	1	JN0006	nerve growth factor r	4.18e-08
4	146	4.7	461	2	JC4302	tumor necrosis factor	4.18e-08
5	142	4.6	454	1	GQMST1	tumor necrosis factor	1.95e-07
6	142	4.6	454	2	I57826	tumor necrosis factor	1.95e-07
7	143	4.6	455	1	GQHUT1	tumor necrosis factor	1.33e-07
8	136	4.4	435	2	I54182	tumor necrosis factor	1.90e-06
9	133	4.3	314	2	I37383	FAS soluble protein -	5.85e-06
10	133	4.3	335	2	A40036	apoptosis-mediating s	5.85e-06
11	130	4.2	326	1	GQVZML	T2 protein - myxoma v	1.77e-05
12	130	4.2	461	1	GQRTT1	tumor necrosis factor	1.77e-05
13	127	4.1	327	2	A46484	apoptosis-mediating m	5.31e-05
14	128	4.1	349	2	D36858	gene G4R protein - va	3.69e-05
15	126	4.1	459	2	I48854	gene murine tumour ne	7.63e-05
16	126	4.1	1192	2	S69000	laminin gamma 2 chain	7.63e-05
17	125	4.0	255	2	JT0752	lymphocyte activation	1.09e-04
18	125	4.0	255	2	I38426	4-1BB - human	1.09e-04
19	125	4.0	474	2	B38634	tumor necrosis factor	1.09e-04
20	122	3.9	324	2	JC2395	Fas antigen precursor	3.20e-04
21	122	3.9	425	1	A26431	nerve growth factor r	3.20e-04
22	121	3.9	427	1	GQHUN	nerve growth factor r	4.57e-04
23	120	3.9	461	1	A35356	tumor necrosis factor	6.50e-04
24	122	3.9	1111	2	B44018	laminin B2t chain - h	3.20e-04
25	122	3.9	1193	2	A44018	laminin B2t chain pre	3.20e-04
26	115	3.7	1680	2	A43434	furin (EC 3.4.21.75)	3.71e-03
27	111	3.6	277	2	A60771	B-cell activation pro	1.45e-02
28	110	3.5	3075	2	S14458	laminin alpha-1 chain	2.02e-02
29	108	3.5	3084	1	MMMSA	laminin alpha-1 chain	3.93e-02
30	107	3.4	250	1	A49053	CD27 antigen precurso	5.46e-02
31	105	3.4	256	2	B32393	T-cell antigen 4-1BB	1.05e-01
32	106	3.4	277	2	I37552	OX40 homolog - human	7.58e-02
33	105	3.4	349	2	T06680	hypothetical protein	1.05e-01
34	105	3.4	493	2	JC5486	membrane glycoprotein	1.05e-01
35	106	3.4	703	2	A49994	sulfate transporter,	7.58e-02
36	107	3.4	1548	2	S34583	serine proteinase (EC	5.46e-02
37	106	3.4	2871	2	A55624	fibrillin-1 precursor	7.58e-02
38	104	3.3	260	1	A46517	CD27 antigen precurso	1.45e-01
39	104	3.3	289	2	A46515	B cell-associated sur	1.45e-01
40	104	3.3	305	2	A46476	CD40 - mouse	1.45e-01
41	103	3.3	596	2	A45664	variant-specific surf	2.00e-01
42	104	3.3	956	1	A46016	thrombospondin 3 - mo	1.45e-01
43	103	3.3	2871	2	A55567	fibrillin I - bovine	2.00e-01
44	103	3.3	3635	2	T10053	laminin alpha 5 chain	2.00e-01
45	101	3.2	1607	1	MMMSB2	laminin gamma-1 chain	3.77e-01

ALIGNMENTS

RESULT 1
ENTRY I48700 #type complete
TITLE gene ox40 protein - mouse
ALTERNATE_NAMES OX40 antigen
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Oct-1996
ACCESSIONS I48700; I48334; S34377
REFERENCE I48700
#authors Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.; Fell, H.P.
#journal J. Immunol. (1993) 151:5261-5271
#title Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell interactions.
#cross-references MUID:94044750
#accession I48700
##status translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues 1-272 ##label RES
##cross-references EMBL:Z21674; NID:g312827; PID:g312828
REFERENCE I48334
#authors Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
#journal Eur. J. Immunol. (1995) 25:926-930
#title Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.
#cross-references MUID:95255413
#accession I48334
##status translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues 1-14,'G',16-272 ##label RE2
##cross-references EMBL:X85214; NID:g732818; PID:g732819
GENETICS
#gene ox40
#introns 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
SUMMARY #length 272 #molecular-weight 30153 #checksum 841

Query Match 5.5%; Score 170; DB 2; Length 272;
Best Local Similarity 27.3%; Pred. No. 2.81e-12;
Matches 48; Conservative 36; Mismatches 78; Indels 14; Gaps 11;

```
Db       9 TALLLLA-LVLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVSRCD--HTRDTLCHP 62
           | |:||: |:  ||    :|  : :   : :|  | :| ||  :   |      |: | :
Qy      15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db      63 CETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLG 120
           |    ::|   :: || | :|   :  : | ||::| |::|  | ||   :    |:
```

```
Qy      75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQ-D 132

Db     121 VDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CED-RSLLATLL 174
           ::|||| | :| : | : | :  : : |  :| || |   ::| :||
Qy     133 MECVPC--GDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALATVLLALL 186


RESULT    2
ENTRY             S12783     #type complete
TITLE             OX40 antigen precursor - rat
ALTERNATE_NAMES   nerve growth factor receptor homolog
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                    20-Sep-1999
ACCESSIONS        S12783; S08036
REFERENCE         S12783
   #authors       Mallett, S.; Fossum, S.; Barclay, A.N.
   #journal       EMBO J. (1990) 9:1063-1068
   #title         Characterization of the MRC OX40 antigen of activated CD4
                    positive T lymphocytes - a molecule related to nerve growth
                    factor receptor.
   #cross-references MUID:90214614
   #accession     S12783
      ##molecule_type mRNA
      ##residues      1-271 ##label MAL
      ##cross-references EMBL:X17037; NID:g57830; PID:g57831
CLASSIFICATION    #superfamily CD27 antigen; NGF receptor repeat homology
KEYWORDS          growth factor receptor; transmembrane protein
FEATURE
   1-19                #domain signal sequence #status predicted #label SIG\
   20-271              #product OX40 antigen #status predicted #label MAT\
   211-235             #domain transmembrane #status predicted #label TMM
SUMMARY           #length 271  #molecular-weight 29895  #checksum 379

  Query Match             4.8%;  Score 149;  DB 2;  Length 271;
  Best Local Similarity  29.1%;  Pred. No. 1.30e-08;
  Matches    39;  Conservative   27;  Mismatches  57;  Indels  11;  Gaps   8;

Db       9 TAFLLLG-LSLGVTVKL-NCVKDTYPS-GHKC--CRECQPGHGMVSRCD--HTRDTVCHP 61
           | ::||| ||  ||    :|  : :   : :|  | :| ||  :   |      |: | :
Qy      15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db      62 CEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQPRQDSSHKLGV 120
           |    ::|   :: || | :|   :  : | ||::| |::| :| ||   :       :
Qy      75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQDM 133

Db     121 DCVPC--PPGHFSP 132
           :|||| || : |
Qy     134 ECVPCGDPPPPYEP 147


RESULT    3
ENTRY             JN0006     #type complete
TITLE             nerve growth factor receptor, low affinity precursor -
                    chicken
ALTERNATE_NAMES   NGF receptor
ORGANISM          #formal_name Gallus gallus #common_name chicken
DATE              10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                    10-Sep-1999
ACCESSIONS        JN0006; A60504
REFERENCE         JN0006
   #authors       Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko,
                    T.P.; Shooter, E.M.; Reichardt, L.F.
   #journal       Neuron (1989) 2:1123-1134
   #title         Structure and developmental expression of the nerve growth
                    factor receptor in the chicken central nervous system.
   #cross-references MUID:90166579
   #accession     JN0006
      ##molecule_type mRNA
      ##residues      1-416 ##label LAR
      ##experimental_source embryonic chick brain
REFERENCE         A60504
   #authors       Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
   #journal       Dev. Biol. (1990) 137:287-304
   #title         Structure and developmental expression of the chicken NGF
                    receptor.
   #cross-references MUID:90152140
   #accession     A60504
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type mRNA
      ##residues      21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416
                       ##label HEU
COMMENT           This receptor is found on sensory and sympathetic neurons, on
                    neuroblastoma cells, and on a variety of nonneuronal derivatives
                    of the neural crest.
COMMENT           The cysteine-rich region of the extracellular domain may form part
                    or all of the NGF-binding site.
COMMENT           This protein is thought to form a high-affinity receptor when it
                    associates with the 140K trk proto-oncogene, which contains an
                    intracellular tyrosine kinase domain.
CLASSIFICATION    #superfamily nerve growth factor receptor; NGF receptor
                    repeat homology
KEYWORDS          duplication; glycoprotein; heterodimer; monomer;
                    phosphoprotein; receptor; transmembrane protein
FEATURE
   1-20                #domain signal sequence #status predicted #label SIG\
   21-416              #product nerve growth factor receptor #status predicted
                         #label MAT\
   21-239              #domain extracellular #status predicted #label EXT\
   24-57               #domain NGF receptor repeat homology #label NG1\
   59-100              #domain NGF receptor repeat homology #label NG2\
   101-139             #domain NGF receptor repeat homology #label NG3\
   141-181             #domain NGF receptor repeat homology #label NG4\
   189-237             #region serine/threonine-rich\
   240-261             #domain transmembrane #status predicted #label MEM\
   262-416             #domain intracellular #status predicted #label INT\
   52                  #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 416  #molecular-weight 44654  #checksum 3542

  Query Match             4.7%;  Score 146;  DB 1;  Length 416;
  Best Local Similarity  30.0%;  Pred. No. 4.18e-08;
  Matches    54;  Conservative   29;  Mismatches  83;  Indels  14;  Gaps  13;

Db      90 PC-VESDDAVCRCAYGYFQDELSGSCKECSICEVGFGLMFPCR-D-SQDTVCEECPEGTF 146
           :| |  : :.||     |:|  ||:|  |: | |  |  |    ::|: | |    |
Qy      24 SCKVTCESGDCR-QQE-FRDR-SGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRF 80

Db     147 SDEANFVDPCLPCTICEENEVMVK-ECTATSDAECRDLHPRWTTHTPSLAGSDSPEPITR 205
            ::  | : | ||  |   :   | :|:||||| | |  |     |  | | :  | :
Qy      81 KEDWGF-QKCKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKT-KLVGFQDMECVPC 138

Db     206 DPFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPVYCSILAAVVVGL-VAYIAF-KR 263
                   |  |  |: :| :  :| ||  | :| || ||:|:::| :  : : ||
Qy     139 GD-PPPPYEPHCASKVNLVKIASTASSPRDTA--LAAVICSALATVLLALLILCVIYCKR 195


RESULT    4
ENTRY             JC4302     #type complete
TITLE             tumor necrosis factor receptor p55 precursor - pig
ORGANISM          #formal_name Sus scrofa domestica #common_name domestic pig
DATE              29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change
                    23-Jul-1999
ACCESSIONS        JC4302; PC4093
REFERENCE         JC4302
   #authors       Suter, B.; Pauli, U.
   #journal       Gene (1995) 163:263-266
   #title         Cloning of the cDNA encoding the porcine p55 tumor necrosis
                    factor receptor.
   #cross-references MUID:96011645
   #accession     JC4302
      ##molecule_type mRNA
      ##residues      1-461 ##label SUT
      ##cross-references GB:U19994; NID:g1141752; PIDN:AAC48499.1;
                         PID:g1141753
   #accession     PC4093
```

```
      ##molecule_type protein
      ##residues       1-7 ##label SU2
      ##experimental_source kidney cell line 15
GENETICS
   #gene          tnfr
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          glycoprotein; kidney; receptor; transmembrane protein; tumor
FEATURE
   1-29                #domain signal sequence #status predicted #label SIG\
   30-461              #product tumor necrosis factor receptor p55 #status
                         predicted #label MAT\
   44-194              #domain extracellular cysteine rich #status predicted
                         #label EXT\
   44-82               #domain NGF receptor repeat homology #label NG1\
   84-126              #domain NGF receptor repeat homology #label NGF\
   211-231             #domain transmembrane #status predicted #label TMM\
   361-447             #domain signal transduction #status predicted #label
                         SIT\
   54,145,151          #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 461  #molecular-weight 50696  #checksum 8079

  Query Match             4.7%;  Score 146;  DB 2;  Length 461;
  Best Local Similarity  25.5%;  Pred. No. 4.18e-08;
  Matches    28;  Conservative   22;  Mismatches  55;  Indels   5;  Gaps   5;

Db      44 CPQGKYSHPQNRSICCTKCHKGTYLHNDC-LGPGLDTDCRECDNGTFTASENHLTQCLSC 102
           | |  :        : |  |  |  | ::| :| | |::|  |    |   :  :  | :|
Qy      34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPC 92

Db     103 SKCRSEMSQVEISPCTVDRDTVCG-CRKNQYRKYWSETLFQCLNCSLCPN 151
             | : ::: : : |:   |::|| |    |||      || ::|  | :
Qy      93 LDC-AVVNRFQKANCSATSDAICGDCLPGFYRKT-KLVGFQDMECVPCGD 140


RESULT    5
ENTRY             GQMST1     #type complete
TITLE             tumor necrosis factor receptor 1 precursor - mouse
ALTERNATE_NAMES   tumor necrosis factor receptor, 55K
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    22-Jun-1999
ACCESSIONS        A38634; B40254; S16677; S19021; I54532
REFERENCE         A38634
   #authors       Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice,
                    G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834
   #title         Cloning and expression of cDNAs for two distinct murine tumor
                    necrosis factor receptors demonstrate one receptor is
                    species specific.
   #cross-references MUID:91187885
   #accession     A38634
      ##molecule_type mRNA
      ##residues       1-454 ##label LEW
      ##cross-references GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
REFERENCE         A40254
   #authors       Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan,
                    C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.
   #journal       Mol. Cell. Biol. (1991) 11:3020-3026
   #title         Molecular cloning and expression of the type 1 and type 2
                    murine receptors for tumor necrosis factor.
   #cross-references MUID:91246168
   #accession     B40254
      ##molecule_type mRNA
      ##residues       1-454 ##label GO2
      ##cross-references GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
REFERENCE         S16677
   #authors       Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis,
                    A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.
   #journal       Eur. J. Immunol. (1991) 21:1649-1656
   #title         Cloning, expression and cross-linking analysis of the murine
                    p55 tumor necrosis factor receptor.
   #cross-references MUID:91285014
   #accession     S16677
      ##molecule_type mRNA
      ##residues       1-454 ##label BAR
      ##cross-references EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
REFERENCE         S19021
   #authors       Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
   #journal       Immunogenetics (1991) 34:338-340
   #title         Molecular cloning and expression of the mouse Tnf receptor
                    type b.
   #cross-references MUID:92039815
   #accession     S19021
      ##molecule_type mRNA
      ##residues       1-454 ##label ROT
      ##cross-references EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
REFERENCE         I54532
   #authors       Bebo, B.F.
   #journal       Immunogenetics (1994) 39:450-451
   #title         Nucleotide sequence of the TNF type I receptor from a mouse
                    endothelioma cell line.
   #cross-references MUID:94245292
   #accession     I54532
      ##status         translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-454 ##label RES
      ##cross-references GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
COMMENT     This protein is one of two distantly related receptors for both
              TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29                #domain signal sequence #status predicted #label SIG\
   30-454              #product tumor necrosis factor receptor type 1 #status
                         predicted #label MAT\
   30-212              #domain extracellular #status predicted #label EXT\
   44-82               #domain NGF receptor repeat homology #label NG1\
   84-126              #domain NGF receptor repeat homology #label NG2\
   127-167             #domain NGF receptor repeat homology #label NG3\
   168-204             #domain NGF receptor repeat homology #label NG4\
   213-235             #domain transmembrane #status predicted #label MEM\
   236-454             #domain intracellular #status predicted #label INT\
   54,151,202          #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 454  #molecular-weight 50129  #checksum 4839

  Query Match             4.6%;  Score 142;  DB 1;  Length 454;
  Best Local Similarity  26.9%;  Pred. No. 1.95e-07;
  Matches    29;  Conservative   16;  Mismatches  58;  Indels   5;  Gaps   5;

Db      44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCPSP-GRDTVCRECEKGTFTASQNYLRQCLSC 102
           | |  :     | : |  |  |  |  :|    | |: |  |    |     : : | :|
Qy      34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGFQK-CKPC 92

Db     103 KTCRKEMSQVEISPCQADKDTVCG-CKENQFQRYLSETHFQCVDCSPC 149
             |   ::: : : | |  |::|| |    | |      || ::| ||
Qy      93 LDCA-VVNRFQKANCSATSDAICGDCLPG-FYRKTKLVGFQDMECVPC 138


RESULT    6
ENTRY             I57826     #type complete
TITLE             tumor necrosis factor receptor - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
                    23-Jul-1999
ACCESSIONS        I57826
REFERENCE         I57826
   #authors       Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.;
                    Steinmetz, M.
   #journal       Mol. Immunol. (1993) 30:165-176
   #title         Genomic organization and promoter function of the murine
                    tumor necrosis factor receptor beta gene.
   #cross-references MUID:93156721
```

```
   #accession    I57826
      ##status        preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues      1-454 ##label RES
      ##cross-references GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
GENETICS
   #gene          TNFR-2
   #introns       13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
CLASSIFICATION    #superfamily tumor necrosis factor receptor type 1; NGF
                    receptor repeat homology
KEYWORDS          cytokine receptor
FEATURE
   44-82               #domain NGF receptor repeat homology #label NGF
SUMMARY           #length 454  #molecular-weight 50030  #checksum 4267

  Query Match             4.6%;  Score 142;  DB 2;  Length 454;
  Best Local Similarity  26.9%;  Pred. No. 1.95e-07;
  Matches    29;  Conservative   16;  Mismatches  58;  Indels   5;  Gaps   5;

Db     44 CPQGKYVHSKNNSICCTKCHKGTYLVSDCPSP-GRDTVCRECEKGTFTASQNYLRQCLSC 102
          | |  :     | : |  |  |  |  :|    | |: |  |    |     : : | :|
Qy     34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGFQK-CKPC 92

Db    103 KTCRKEMSQVEISPCQADKDTVCG-CKENQFQRYLSETHFQCVDCSPC 149
          |   ::: : : | |  |::|| |    | |       || ::| ||
Qy     93 LDCA-VVNRFQKANCSATSDAICGDCLPG-FYRKTKLVGFQDMECVPC 138


RESULT    7
ENTRY             GQHUT1     #type complete
TITLE             tumor necrosis factor receptor 1 precursor - human
ALTERNATE_NAMES   P55 tumor necrosis factor receptor; TNF receptor
CONTAINS          tumor necrosis factor alpha inhibitor; tumor necrosis factor
                    binding protein 1 (TNF blocking factor)
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                    22-Jun-1999
ACCESSIONS        A38208; A34899; A34900; A36555; C36555; A38281; S12057;
                    JT0758; A60231; A38258; A60594; A35010; JC2404
REFERENCE         A38208
   #authors       Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
   #journal       Genomics (1992) 13:219-224
   #title         Structure of the human TNF receptor 1 (p60) gene (TNRF1) and
                    localization to chromosome 12p13.
   #cross-references MUID:92250049
   #accession    A38208
      ##molecule_type DNA
      ##residues      1-455 ##label FUC
      ##cross-references GB:M75864; GB:M75865; GB:M75866; NID:g339748;
                        PIDN:AAA61201.1; PID:g339750
REFERENCE         A34899
   #authors       Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus,
                    M.; Tabuchi, H.; Lesslauer, W.
   #journal       Cell (1990) 61:351-359
   #title         Molecular cloning and expression of the human 55 kd tumor
                    necrosis factor receptor.
   #cross-references MUID:90235284
   #accession    A34899
      ##molecule_type mRNA
      ##residues      1-455 ##label LOE
      ##cross-references GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1;
                        PID:g339754
      ##experimental_source placenta
      ##note          part of this sequence, including the amino end of the
                       mature protein, confirmed by protein sequencing
REFERENCE         A34900
   #authors       Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.;
                    Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab,
                    H.; Kohr, W.J.; Goeddel, D.V.
   #journal       Cell (1990) 61:361-370
   #title         Molecular cloning and expression of a receptor for human
                    tumor necrosis factor.
   #cross-references MUID:90235285
   #accession    A34900
      ##molecule_type mRNA
      ##residues      1-455 ##label SCH
      ##cross-references GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
REFERENCE         A36555
   #authors       Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                    Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                    Stratowa, C.; Adolf, G.R.
   #journal       DNA Cell Biol. (1990) 9:705-715
   #title         Molecular cloning and expression of human and rat tumor
                    necrosis factor receptor chain (p60) and its soluble
                    derivative, tumor necrosis factor-binding protein.
   #cross-references MUID:91090841
   #accession    A36555
      ##molecule_type mRNA
      ##residues      1-455 ##label HIM
      ##cross-references GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
   #accession    C36555
      ##molecule_type protein
      ##residues      30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;
                       107-128;162-167,'X',169-201 ##label HI2
      ##note          the purified protein, called tumor necrosis factor
                       binding protein, is a soluble derivative of the
                       receptor
REFERENCE         A38281
   #authors       Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
                    M.
   #journal       Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
   #title         Cloning of human tumor necrosis factor (TNF) receptor cDNA
                    and expression of recombinant soluble TNF-binding protein.
   #cross-references MUID:91017509
   #accession    A38281
      ##molecule_type mRNA
      ##residues      1-455 ##label GRA
      ##cross-references GB:M37764
      ##note          the authors translated the codon TGG for residue 371 as
                       Thr, AAG for residue 372 as Leu, and GAC for residue
                       427 as Asn
REFERENCE         S12057
   #authors       Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
                    R.; Aderka, D.; Holtmann, H.; Wallach, D.
   #journal       EMBO J. (1990) 9:3269-3278
   #title         Soluble forms of tumor necrosis factor receptors (TNF-Rs).
                    The cDNA for the type I TNF-R, cloned using amino acid
                    sequence data of its soluble form, encodes both the cell
                    surface and a soluble form of the receptor.
   #cross-references MUID:91006021
   #accession    S12057
      ##molecule_type mRNA
      ##residues      1-455 ##label NOP
      ##cross-references EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
      ##note          parts of soluble TNF binding protein 1, including its
                       amino and carboxyl ends, were confirmed by protein
                       sequencing
REFERENCE         JT0758
   #authors       Kemper, O.; Wallach, D.
   #journal       Gene (1993) 134:209-216
   #title         Cloning and partial characterization of the promoter for the
                    human p55 tumor necrosis factor (TNF) receptor.
   #cross-references MUID:94085779
   #accession    JT0758
      ##molecule_type DNA
      ##residues      1-13 ##label KEM
REFERENCE         A60231
   #authors       Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
                    J.M.
   #journal       Eur. J. Immunol. (1990) 20:1167-1174
   #title         Tumor necrosis factor inhibitor: purification, NH-2-terminal
                    amino acid sequence and evidence for anti-inflammatory and
                    immunomodulatory activities.
   #cross-references MUID:90292116
   #accession    A60231
      ##molecule_type protein
```

```
     ##residues      41-43,'X',45-53,'X',55-57 ##label SEC
REFERENCE        A38258
   #authors      Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III,
                   J.A.; Jeffes, E.W.B.; Lentz, R.; Tomich, J.; Yamamoto,
                   R.S.; Granger, G.A.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
   #title        Purification and characterization of an inhibitor (soluble
                   tumor necrosis factor receptor) for tumor necrosis factor
                   and lymphotoxin obtained from the serum ultrafiltrates of
                   human cancer patients.
   #cross-references MUID:91062364
   #accession    A38258
      ##molecule_type protein
      ##residues      41-60 ##label GAT
      ##experimental_source cancer patient serum
REFERENCE        A60594
   #authors      Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
                   Grubb, A.; Adolf, G.
   #journal      Eur. J. Haematol. (1989) 42:270-275
   #title        Isolation and characterization of a tumor necrosis factor
                   binding protein from urine.
   #cross-references MUID:89171156
   #accession    A60594
      ##molecule_type protein
      ##residues      41-43,'X',45-53,'V',55-57,'XK',60 ##label OLS
      ##experimental_source renal failure patient urine
REFERENCE        A35010
   #authors      Engelmann, H.; Novick, D.; Wallach, D.
   #journal      J. Biol. Chem. (1990) 265:1531-1536
   #title        Two tumor necrosis factor-binding proteins purified from
                   human urine. Evidence for immunological cross-reactivity
                   with cell surface tumor necrosis factor receptors.
   #cross-references MUID:90110215
   #accession    A35010
      ##molecule_type protein
      ##residues      41-45 ##label ENG
      ##experimental_source normal urine
REFERENCE        JC2404
   #authors      Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
   #journal      Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
   #title        Amino acid sequence of natural tumor necrosis factor alpha
                   inhibitor purified from human urine.
   #cross-references MUID:95128033
   #accession    JC2404
      ##molecule_type protein
      ##residues      41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201
                        ##label KAJ
      ##experimental_source urine
COMMENT     This protein is one of two known receptors for both TNF-alpha
              (cachectin) and TNF-beta (lymphotoxin).
GENETICS
   #gene         GDB:TNFR1
      ##cross-references GDB:125913; OMIM:191190
   #map_position 12p13.2-12p13.2
   #introns      13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION   #superfamily tumor necrosis factor receptor type 1; NGF
                   receptor repeat homology
KEYWORDS         duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-21              #domain signal sequence #status predicted #label SIG\
   22-455            #product tumor necrosis factor receptor type 1 #status
                       predicted #label MAT\
   30-211            #domain extracellular #status predicted #label EXT\
   41-201            #product TNF binding protein 1 (tumor necrosis factor
                       alpha inhibitor) #status experimental #label TBP1\
   44-82             #domain NGF receptor repeat homology #label NG1\
   84-126            #domain NGF receptor repeat homology #label NG2\
   127-167           #domain NGF receptor repeat homology #label NG3\
   168-196           #domain NGF receptor repeat homology #label NG4\
   212-234           #domain transmembrane #status predicted #label MEM\
   235-455           #domain intracellular #status predicted #label INT\
   54,145,151        #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
```

```
SUMMARY          #length 455  #molecular-weight 50494  #checksum 153

  Query Match             4.6%;  Score 143;  DB 1;  Length 455;
  Best Local Similarity  25.2%;  Pred. No. 1.33e-07;
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db      11 LPL-VLLELEVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
           ::| |||| . :: : :: |: |: :   :| | |  :     | : |  |  |  |
Qy       1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db      69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
            ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::||
Qy      59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db     127 CRKNQYR 133
           |   ||
Qy     117 CLPGFYR 123


RESULT    8
ENTRY            I54182     #type complete
TITLE            tumor necrosis factor receptor 2-related protein - human
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             24-May-1996 #sequence_revision 24-May-1996 #text_change
                   29-Aug-1997
ACCESSIONS       I54182
REFERENCE        I54182
   #authors      Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.;
                   Marynen, P.
   #journal      Genomics (1993) 16:214-218
   #title        Construction and evaluation of a hncDNA library of human 12p
                   transcribed sequences derived from a somatic cell hybrid.
   #cross-references MUID:93252381
   #accession    I54182
      ##status       preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues      1-435 ##label RES
      ##cross-references GB:L04270; NID:g339761; PID:g339762
GENETICS
   #gene         GDB:LTBR
      ##cross-references GDB:1230195; OMIM:600979
   #map_position 12p13.3-12p13.1
SUMMARY          #length 435  #molecular-weight 46709  #checksum 63

  Query Match             4.4%;  Score 136;  DB 2;  Length 435;
  Best Local Similarity  26.3%;  Pred. No. 1.90e-06;
  Matches    26;  Conservative   24;  Mismatches  41;  Indels   8;  Gaps   8;

Db      37 ASENQTCRDQEKEYYE-PQHRICCSRCPPGTYVSAKCS-RI-RDTVCATCAENSYNEHWN 93
           : |:  || |: |: : : : : :|::| ||  :|  |:     |: | :|  : ::| |
Qy      28 TCESGDCR-QQ-EFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG 85

Db      94 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQC-RCQPGMF 131
           :   |  |  |  |  ::  | |::   : |  | || :
Qy      86 FQK-CKPCLDCAVVNRFQK-ANCSATSDAICGDCLPGFY 122


RESULT    9
ENTRY            I37383     #type complete
TITLE            FAS soluble protein - human
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                   02-Jul-1996
ACCESSIONS       I37383
REFERENCE        I37383
   #authors      Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
   #journal      J. Immunol. (1995) 154:2706-2713
   #title        Three functional soluble forms of the human
                   apoptosis-inducing Fas molecule are produced by alternative
                   splicing.
   #cross-references MUID:95181785
   #accession    I37383
      ##status       preliminary; translated from GB/EMBL/DDBJ
```

```
      ##molecule_type mRNA
      ##residues      1-314 ##label RES
      ##cross-references EMBL:Z47993; NID:g728578; PID:g695539
SUMMARY          #length 314  #molecular-weight 35386  #checksum 655

  Query Match            4.3%;  Score 133;  DB 2;  Length 314;
  Best Local Similarity  26.9%;  Pred. No. 5.85e-06;
  Matches    21;  Conservative   21;  Mismatches  30;  Indels   6;  Gaps   6;

Db     59 CHKPCPPGERKARDCTVN-GDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEI 117
          |:  | ||   :::|    |::::||:|:  : : :   |  ||: |  |   : ::
Qy     49 CNQ-CGPGMELSKECGFGYGEDAQCVACRLHR-FKEDWGFQ-KCKPCLDCAVVNRFQ-KA 104

Db    118 NCTRTQNTKC-RCKPNFF 134
          ||: | :: |  | | |:
Qy    105 NCSATSDAICGDCLPGFY 122


RESULT   10
ENTRY            A40036     #type complete
TITLE            apoptosis-mediating surface antigen Fas precursor - human
ALTERNATE_NAMES  surface antigen APO-1
ORGANISM         #formal_name Homo sapiens #common_name man
DATE             17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change
                   10-Sep-1997
ACCESSIONS       A40036; S24543; A38142
REFERENCE        A40036
   #authors      Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima,
                   S.I.; Sameshima, M.; Hase, A.; Seto, Y.; Nagata, S.
   #journal      Cell (1991) 66:233-243
   #title        The polypeptide encoded by the cDNA for human cell surface
                   antigen Fas can mediate apoptosis.
   #cross-references MUID:91309137
   #accession    A40036
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-335 ##label ITO
      ##cross-references GB:M67454; NID:g182409; PID:g182410
REFERENCE        S24543
   #authors      Krammer, P.H.
   #submission   submitted to the EMBL Data Library, February 1992
   #accession    S24543
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-335 ##label KRA
      ##cross-references EMBL:X63717; NID:g28741; PID:g28742
REFERENCE        A38142
   #authors      Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.;
                   Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauth,
                   B.C.; Ponsting, H.; Krammer, P.H.
   #journal      J. Biol. Chem. (1992) 267:10709-10715
   #title        Purification and molecular cloning of the APO-1 cell surface
                   antigen, a member of the tumor necrosis factor/nerve growth
                   factor receptor superfamily. Sequence identity with the Fas
                   antigen.
   #cross-references MUID:92268122
   #accession    A38142
      ##status        preliminary; not compared with conceptual translation
      ##molecule_type nucleic acid
      ##residues      1-134,'Q',136-335 ##label OEH
      ##experimental_source SKW6.4 cells
      ##note          sequence extracted from NCBI backbone (NCBIP:103810)
      ##note          in NCBI backbone the source is designated as mouse
GENETICS
   #gene         GDB:APT1
      ##cross-references GDB:132671; OMIM:134637
   #map_position 10q24.1-10q24.1
CLASSIFICATION   #superfamily NGF receptor repeat homology
KEYWORDS         apoptosis; surface antigen; transmembrane protein
FEATURE
   1-16              #domain signal sequence #status predicted #label SIG\
   85-128            #domain NGF receptor repeat homology #label NG4\
   174-190           #domain transmembrane #status predicted #label TMM
SUMMARY          #length 335  #molecular-weight 37732  #checksum 4899

  Query Match            4.3%;  Score 133;  DB 2;  Length 335;
  Best Local Similarity  26.9%;  Pred. No. 5.85e-06;
  Matches    21;  Conservative   21;  Mismatches  30;  Indels   6;  Gaps   6;

Db     59 CHKPCPPGERKARDCTVN-GDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEI 117
          |:  | ||   :::|    |::::||:|:  : : :   |  ||: |  |   : ::
Qy     49 CNQ-CGPGMELSKECGFGYGEDAQCVACRLHR-FKEDWGFQ-KCKPCLDCAVVNRFQ-KA 104

Db    118 NCTRTQNTKC-RCKPNFF 134
          ||: | :: |  | | |:
Qy    105 NCSATSDAICGDCLPGFY 122


RESULT   11
ENTRY            GQVZML     #type complete
TITLE            T2 protein - myxoma virus (strain Lausanne)
ORGANISM         #formal_name myxoma virus
DATE             31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
                   18-Jun-1999
ACCESSIONS       A40566
REFERENCE        A40566
   #authors      Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.
   #journal      Virology (1991) 184:370-382
   #title        Myxoma virus expresses a secreted protein with homology to
                   the tumor necrosis factor receptor gene family that
                   contributes to viral virulence.
   #cross-references MUID:91335768
   #accession    A40566
      ##molecule_type DNA
      ##residues      1-326 ##label UPT
      ##cross-references GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1;
                        PID:g332310
CLASSIFICATION   #superfamily myxoma virus T2 protein; NGF receptor repeat
                   homology
KEYWORDS         glycoprotein
FEATURE
   64-105            #domain NGF receptor repeat homology #label NG2\
   106-147           #domain NGF receptor repeat homology #label NG3\
   66,181,205,238    #binding_site carbohydrate (Asn) (covalent) #status
                       predicted
SUMMARY          #length 326  #molecular-weight 35208  #checksum 9255

  Query Match            4.2%;  Score 130;  DB 1;  Length 326;
  Best Local Similarity  29.5%;  Pred. No. 1.77e-05;
  Matches    28;  Conservative   16;  Mismatches  42;  Indels   9;  Gaps   8;

Db     24 DRGKCRGNDY-EKDGLC--CTSCPPGSYASRLCG-P-GSDTVCSPCKNETFTASTNHAPA 78
          : | ||  :: :: | |  |  | ||   |: ||   | |: | :|:   |
Qy     30 ESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGF-QK 88

Db     79 CVSCRGRCTG-HLSESQSCDKTRDRVC-DCSAGNY 111
          | :|   |:  :  :  :|  | | :| || :| |
Qy     89 CKPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   12
ENTRY            GQRTT1     #type complete
TITLE            tumor necrosis factor receptor 1 precursor - rat
CONTAINS         tumor necrosis factor binding protein 1 (TNF blocking factor)
ORGANISM         #formal_name Rattus norvegicus #common_name Norway rat
DATE             30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change
                   22-Jun-1999
ACCESSIONS       B36555
REFERENCE        A36555
   #authors      Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
                   Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
                   Stratowa, C.; Adolf, G.R.
   #journal      DNA Cell Biol. (1990) 9:705-715
   #title        Molecular cloning and expression of human and rat tumor
                   necrosis factor receptor chain (p60) and its soluble
                   derivative, tumor necrosis factor-binding protein.
```

```
   #cross-references MUID:91090841
   #accession    B36555
      ##molecule_type mRNA
      ##residues      1-461 ##label HIM
      ##cross-references GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
COMMENT     This protein is one of two known receptors for both TNF-alpha
            (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION   #superfamily tumor necrosis factor receptor type 1; NGF
                   receptor repeat homology
KEYWORDS         duplication; glycoprotein; receptor; transmembrane protein
FEATURE
   1-29               #domain signal sequence #status predicted #label SIG\
   30-461             #product tumor necrosis factor receptor type 1 #status
                        predicted #label MAT\
   30-211             #domain extracellular #status predicted #label EXT\
   30-201             #product tumor necrosis factor binding protein #status
                        predicted #label TBP\
   44-82              #domain NGF receptor repeat homology #label NG1\
   84-126             #domain NGF receptor repeat homology #label NG2\
   127-167            #domain NGF receptor repeat homology #label NG3\
   168-204            #domain NGF receptor repeat homology #label NG4\
   212-234            #domain transmembrane #status predicted #label MEM\
   235-461            #domain intracellular #status predicted #label INT\
   54,151,201         #binding_site carbohydrate (Asn) (covalent) #status
                        predicted
SUMMARY          #length 461  #molecular-weight 50969  #checksum 1617

  Query Match             4.2%;  Score 130;  DB 1;  Length 461;
  Best Local Similarity  25.9%;  Pred. No. 1.77e-05;
  Matches    28;  Conservative   16;  Mismatches  59;  Indels   5;  Gaps   5;

Db     44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSP-GQETVCEVCDKGTFTASQNHVRQCLSC 102
          | |  :     | : |  |  |  |  :|    |::: |  |    |       : | :|
Qy     34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGF-QKCKPC 92

Db    103 KTCRKEMFQVEISPCKADMDTVCG-CKKNQFQRYLSETHFQCVDCSPC 149
            |   : : : : | |  |::|| |    | |      || ::| ||
Qy     93 LDCA-VVNRFQKANCSATSDAICGDCLPG-FYRKTKLVGFQDMECVPC 138


RESULT   13
ENTRY            A46484     #type complete
TITLE            apoptosis-mediating membrane-associated polypeptide Fas -
                   mouse
ORGANISM         #formal_name Mus musculus #common_name house mouse
DATE             18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
                   16-Jul-1999
ACCESSIONS       A46484; A47254
REFERENCE        A46484
   #authors      Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.;
                   Copeland, N.G.; Jenkins, N.A.; Nagata, S.
   #journal      J. Immunol. (1992) 148:1274-1279
   #title        The cDNA structure, expression, and chromosomal assignment of
                   the mouse Fas antigen.
   #cross-references MUID:92148151
   #accession    A46484
      ##status        preliminary
      ##molecule_type mRNA
      ##residues      1-327 ##label WAT
      ##cross-references GB:M83649; NID:g193225; PID:g193226
      ##experimental_source BAM3 macrophage cell line
      ##note          sequence extracted from NCBI backbone (NCBIN:81544,
                       NCBIP:81545)
REFERENCE        A47254
   #authors      Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
   #journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
   #title        Aberrant transcription caused by the insertion of an early
                   transposable element in an intron of the Fas antigen gene
                   of lpr mice.
   #cross-references MUID:93189576
   #accession    A47254
      ##status        preliminary
      ##molecule_type nucleic acid
      ##residues      1-96 ##label ADA
      ##cross-references GB:S56490; NID:g298505; PID:g298506
      ##experimental_source MRL lpr/lpr
      ##note          sequence extracted from NCBI backbone (NCBIN:126850,
                       NCBIN:126853, NCBIN:126863, NCBIP:126864)
CLASSIFICATION   #superfamily NGF receptor repeat homology
KEYWORDS         transmembrane protein
FEATURE
   44-79              #domain NGF receptor repeat homology #label NGF\
   81-124             #domain NGF receptor repeat homology #label NG4
SUMMARY          #length 327  #molecular-weight 37417  #checksum 8479

  Query Match             4.1%;  Score 127;  DB 2;  Length 327;
  Best Local Similarity  26.0%;  Pred. No. 5.31e-05;
  Matches    20;  Conservative   18;  Mismatches  34;  Indels   5;  Gaps   5;

Db     56 CQPCQPGKKKVEDCKMN-GGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETN 114
          |  | ||:    :|    |  : | :|   : :::   : :||: |  |   : ::  :|
Qy     49 CNQCGPGMELSKECGFGYGEDAQCVACRLHR-FKEDWGF-QKCKPCLDCAVVNRFQ-KAN 105

Db    115 CTLTQNTKC-KCKPDFY 130
          |: | :: |  | | ||
Qy    106 CSATSDAICGDCLPGFY 122


RESULT   14
ENTRY            D36858     #type complete
TITLE            gene G4R protein - variola virus
ALTERNATE_NAMES  B23R protein (COP)
ORGANISM         #formal_name variola virus
DATE             30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                   26-Aug-1999
ACCESSIONS       D36858; S46888; S32385; S35987
REFERENCE        A36859
   #authors      Blinov, V.M.
   #submission   submitted to GenBank, November 1992
   #description  not shown.
   #accession    D36858
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-349 ##label BLI
      ##cross-references GB:X69198; NID:g456758; PID:g457087
      ##experimental_source strain India-1967, ssp. major, isolate Ind3
REFERENCE        S46868
   #authors      Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov,
                   S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.;
                   Shchelkunov, S.N.; Sandakhchiev, L.S.
   #submission   submitted to the EMBL Data Library, April 1992
   #description  Nucleotide sequence analysis of the region of variola virus
                   XhoI F O H P Q genome fragment.
   #accession    S46888
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-349 ##label KOL
      ##cross-references EMBL:X67117; NID:g516428; PID:g516449
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REFERENCE        S32385
   #authors      Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
   #journal      FEBS Lett. (1993) 319:80-83
   #title        Genes of variola and vaccinia viruses necessary to overcome
                   the host protective mechanisms.
   #cross-references MUID:93202281
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FEATURE
   32-66              #domain NGF receptor repeat homology #label NGF\
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   110-151            #domain NGF receptor repeat homology #label NG3
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  Best Local Similarity  28.7%;  Pred. No. 3.69e-05;
  Matches    27;  Conservative   21;  Mismatches  37;  Indels   9;  Gaps   8;

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Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKC 89

Db      84 LSCNGRCNS-NQVETRSCNTTHNRIC-ECSPGYY 115
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RESULT   15
ENTRY             I48854     #type fragment
TITLE             gene murine tumour necrosis factor receptor 2 protein - mouse
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ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
                    23-Jul-1999
ACCESSIONS        I48854
REFERENCE         I48854
   #authors       Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
   #journal       Mamm. Genome (1994) 5:726-727
   #title         Allelic variation of the type 2 tumor necrosis factor
                    receptor gene.
   #cross-references MUID:95178848
   #accession     I48854
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues       1-459 ##label RES
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FEATURE
   151-188            #domain NGF receptor repeat homology #label NGF
SUMMARY           #length 459  #checksum 3156

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Search completed: Tue Apr 18 13:59:33 2000
Job time : 63 secs.
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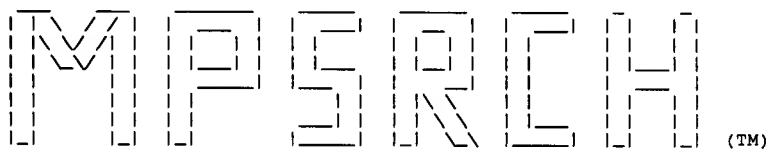

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 18 14:02:47 2000; MasPar time 7.76 Seconds
705.843 Million cell updates/sec

Tabular output not generated.

Title: >US-09-490-187-2
Description: (1-423) from US09490187.pep
Perfect Score: 3111
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....AVIHPATQTSLQVRQRLGSL 423

Scoring table: PAM 150
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 32.744; Variance 152.615; scale 0.215

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	187	6.0	186	1	US-08-089-	Sequence 6, Applicatio	3.49e-06
2	178	5.7	206	1	US-08-494-	Sequence 7, Applicatio	1.81e-05
3	178	5.7	206	1	US-08-097-	Sequence 7, Applicatio	1.81e-05
4	178	5.7	438	1	US-08-097-	Sequence 11, Applicati	1.81e-05
5	178	5.7	438	1	US-08-494-	Sequence 11, Applicati	1.81e-05
6	151	4.9	158	2	US-08-465-	Sequence 54, Applicati	2.27e-03
7	151	4.9	158	1	US-08-050-	Sequence 54, Applicati	2.27e-03
8	148	4.8	139	2	US-08-219-	Sequence 8, Applicatio	3.84e-03
9	148	4.8	355	1	US-08-292-	Sequence 6, Applicatio	3.84e-03
10	147	4.7	154	2	US-08-232-	Sequence 10, Applicati	4.58e-03
11	143	4.6	167	1	US-08-050-	Sequence 57, Applicati	9.20e-03
12	143	4.6	167	2	US-08-465-	Sequence 2, Applicatio	9.20e-03
13	143	4.6	167	1	US-08-050-	Sequence 2, Applicatio	9.20e-03
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15	143	4.6	455	1	US-08-050-	Sequence 25, Applicati	9.20e-03
16	143	4.6	455	2	US-08-465-	Sequence 25, Applicati	9.20e-03
17	143	4.6	455	2	US-08-126-	Sequence 2, Applicatio	9.20e-03
18	143	4.6	455	1	US-08-837-	Sequence 2, Applicatio	9.20e-03
19	143	4.6	455	1	US-08-321-	Sequence 2, Applicatio	9.20e-03
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22	138	4.4	153	2	US-08-219-	Sequence 4, Applicatio	2.19e-02
23	136	4.4	197	2	US-08-505-	Sequence 1, Applicatio	3.09e-02
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ALIGNMENTS

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DE   Sequence 6, Application US/08089458B
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CC    Sequence 6, Application US/08089458B
CC    Patent No. 5359039
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig
CC       APPLICANT:  Goodwin, Raymond
CC       TITLE OF INVENTION:  Isolated Poxvirus A53R-Equivalent Tumor
CC       TITLE OF INVENTION:  Necrosis Factor Antagonists
CC       NUMBER OF SEQUENCES:  7
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Patricia Anne Perkins, Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  U.S.A.
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  Apple Macintosh
CC         OPERATING SYSTEM:  Apple Operating System 7.1
CC         SOFTWARE:  Microsoft Word, Version #5.1a
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/089,458B
CC         FILING DATE:  07/09/93
CC         CLASSIFICATION:  514
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2608
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 233-0644
CC         TELEX:  756822
CC     INFORMATION FOR SEQ ID NO:  6:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  186 amino acids
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Db      90 CHQCRKCPT-GSFDKVKCTGTQNSKCS-CLPGWFCATDSSKTEDCRDCIP 137
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CC    Sequence 7, Application US/08494574
CC    Patent No. 5783665
CC     GENERAL INFORMATION:
CC       APPLICANT:  Baum, Peter
CC       APPLICANT:  Goodwin, Ray
CC       APPLICANT:  Fanslow, William
CC       APPLICANT:  Gayle, Richard
CC       TITLE OF INVENTION:  No. 5783665el Cytokine Which is a Ligand for
CC       TITLE OF INVENTION:  OX40
CC       NUMBER OF SEQUENCES:  13
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  WA
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/494,574
CC         FILING DATE:  22-JUN-1995
CC         CLASSIFICATION:  530
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/097,827
CC         FILING DATE:  23-JUL-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2806
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  206-587-0730
CC      INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  206 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   206 AA; 22939 MW; 232405 CN;

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  Matches    49;  Conservative   36;  Mismatches  77;  Indels  14;  Gaps  11;

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CC    Sequence 7, Application US/08097827
CC    Patent No. 5457035
CC     GENERAL INFORMATION:
CC       APPLICANT:  Baum, Peter
CC       APPLICANT:  Goodwin, Ray
CC       APPLICANT:  Fanslow, William
CC       APPLICANT:  Gayle, Richard
CC       TITLE OF INVENTION:  No. 5457035el Cytokine Which is a Ligand for
CC       TITLE OF INVENTION:  OX40
CC       NUMBER OF SEQUENCES:  13
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  WA
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/097,827
CC         FILING DATE:
CC         CLASSIFICATION:  536
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2806
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  206-587-0730
CC      INFORMATION FOR SEQ ID NO:  7:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  206 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   206 AA; 22939 MW; 232405 CN;

  Query Match           5.7%;  Score 178;  DB 1;  Length 206;
  Best Local Similarity  27.8%;  Pred. No. 1.81e-05;
  Matches    49;  Conservative   36;  Mismatches  77;  Indels  14;  Gaps  11;

Db       9 TALLLLG-LTLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVNRCD--HTRDTLCHP 62
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DE   Sequence 11, Application US/08097827
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CC    Sequence 11, Application US/08097827
CC    Patent No. 5457035
CC     GENERAL INFORMATION:
CC       APPLICANT:  Baum, Peter
CC       APPLICANT:  Goodwin, Ray
CC       APPLICANT:  Fanslow, William
CC       APPLICANT:  Gayle, Richard
CC       TITLE OF INVENTION:  No. 5457035el Cytokine Which is a Ligand for
CC       TITLE OF INVENTION:  OX40
CC       NUMBER OF SEQUENCES:  13
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  WA
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/097,827
CC         FILING DATE:
CC         CLASSIFICATION:  536
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2806
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  206-587-0730
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  438 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   438 AA; 49029 MW; 1097666 CN;

  Query Match           5.7%;  Score 178;  DB 1;  Length 438;
  Best Local Similarity  27.8%;  Pred. No. 1.81e-05;
  Matches    49;  Conservative   36;  Mismatches  77;  Indels  14;  Gaps  11;

Db      9 TALLLLG-LTLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVNRCD--HTRDTLCHP 62
          | |:||| |:  ||    :|  : :   : :|  | :| ||  : : |      |: | :
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DE   Sequence 11, Application US/08494574
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CC    Sequence 11, Application US/08494574
CC    Patent No. 5783665
CC     GENERAL INFORMATION:
CC       APPLICANT:  Baum, Peter
CC       APPLICANT:  Goodwin, Ray
CC       APPLICANT:  Fanslow, William
CC       APPLICANT:  Gayle, Richard
CC       TITLE OF INVENTION:  No. 5783665el Cytokine Which is a Ligand for
CC       TITLE OF INVENTION:  OX40
CC       NUMBER OF SEQUENCES:  13
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  WA
CC         COUNTRY:  USA
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CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/494,574
CC         FILING DATE:  22-JUN-1995
CC         CLASSIFICATION:  530
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/097,827
CC         FILING DATE:  23-JUL-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2806
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  206-587-0730
CC     INFORMATION FOR SEQ ID NO:  11:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  438 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   438 AA; 49029 MW; 1097666 CN;

  Query Match           5.7%;  Score 178;  DB 1;  Length 438;
  Best Local Similarity  27.8%;  Pred. No. 1.81e-05;
  Matches    49;  Conservative   36;  Mismatches  77;  Indels  14;  Gaps  11;

Db      9 TALLLLG-LTLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVNRCD--HTRDTLCHP 62
          | |:||| |:  ||    :|  : :   : :|  | :| ||  : : |      |: | :
Qy     15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db     63 CETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLG 120
          |    ::|   :: || | :|   :  : | ||::| |::|  | ||   :    |:
Qy     75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQ-D 132

Db    121 VDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CED-RSLLATLL 174
          ::|||| | :| :  | : |    : :  |   :| || |    ::| :||
Qy    133 MECVPC--GDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALATVLLALL 186


RESULT    6
ID   US-08-465-982-54     STANDARD;     PRT;   158 AA.
XX
AC   xxxxxx
XX
DT
XX
```

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DE   Sequence 54, Application US/08465982
XX
CC    Sequence 54, Application US/08465982
CC    Patent No. 5863786
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/465,982
CC         FILING DATE:
CC         CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319
CC         FILING DATE:  10-May-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  54:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  158 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   158 AA; 17375 MW; 124033 CN;

  Query Match            4.9%;  Score 151;  DB 2;  Length 158;
  Best Local Similarity  24.6%;  Pred. No. 2.27e-03;
  Matches    31;  Conservative   32;  Mismatches  55;  Indels   8;  Gaps   8;

Db      11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
           ::| ||||    :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy       1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db      69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCT- 126
           ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::|
Qy      59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db     127 CHAGFF 132
           | :||:
Qy     117 CLPGFY 122


RESULT    7
ID   US-08-050-319B-54     STANDARD;     PRT;   158 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 54, Application US/08050319B
XX
CC    Sequence 54, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  54:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  158 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   158 AA; 17375 MW; 124033 CN;

  Query Match            4.9%;  Score 151;  DB 1;  Length 158;
  Best Local Similarity  24.6%;  Pred. No. 2.27e-03;
  Matches    31;  Conservative   32;  Mismatches  55;  Indels   8;  Gaps   8;

Db      11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
           ::| ||||    :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy       1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db      69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCT- 126
           ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::|
Qy      59 SKECGFGYGFDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db     127 CHAGFF 132
           | :||:
Qy     117 CLPGFY 122


RESULT    8
ID   US-08-219-237B;8     STANDARD;     PRT;   139 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 8, Application US/08219237B
XX
CC    Sequence 8, Application US/08219237B
CC    Patent No. 5874546
CC     GENERAL INFORMATION:
CC       APPLICANT:  NAGATA, Shigekazu
CC       APPLICANT:  ITOH, Naoto
CC       APPLICANT:  YONEHARA, Shin
CC       TITLE OF INVENTION:  DNA Coding for Human Cell Surface Antigen
CC       NUMBER OF SEQUENCES:  11
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  James W. Hellwege
CC         STREET:  P.O. Box 2266 Eads Station
```

```
CC         CITY:  Arlington
CC         STATE:  Virginia
CC         COUNTRY:  USA
CC         ZIP:  22202
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/219,237B
CC         FILING DATE:  28-MAR-1994
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US 07/872,129
CC         FILING DATE:  22-APR-1992
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  James W. Hellwege
CC         REGISTRATION NUMBER:  28,808
CC         REFERENCE/DOCKET NUMBER:  516762
CC     INFORMATION FOR SEQ ID NO:  8:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  139 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   139 AA; 15298 MW; 98625 CN;

  Query Match             4.8%;  Score 148;  DB 2;  Length 139;
  Best Local Similarity  29.0%;  Pred. No. 3.84e-03;
  Matches    29;  Conservative   20;  Mismatches  45;  Indels   6;  Gaps   4;

Db     13 CRECQPGHGMVSRCD--HTRDTVCHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCT 70
           | :| ||   :   |       |: | :|    ::|   :: || | :|   :  : | ||:
Qy     49 CNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCS 107

Db     71 PTEDTVC-QCRPGTQPRQDSSHKLGVDCVPC--PPGHFSP 107
          :| |:::| :| ||   :        ::|||| ||  : |
Qy    108 ATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEP 147


RESULT    9
ID   US-08-292-549-6     STANDARD;     PRT;   355 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 6, Application US/08292549
XX
CC    Sequence 6, Application US/08292549
CC    Patent No. 5464938
CC     GENERAL INFORMATION:
CC       APPLICANT:  Smith, Craig A.
CC       APPLICANT:  Goodwin, Raymond G.
CC       TITLE OF INVENTION:  Isolated Viral Protein TNF Antagonists
CC       NUMBER OF SEQUENCES:  10
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Immunex Corporation
CC         STREET:  51 University Street
CC         CITY:  Seattle
CC         STATE:  Washington
CC         COUNTRY:  USA
CC         ZIP:  98101
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/292,549
CC         FILING DATE:
CC         CLASSIFICATION:  530
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  07/963,330
CC         FILING DATE:  10/19/92
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Perkins, Patricia A.
CC         REGISTRATION NUMBER:  34,693
CC         REFERENCE/DOCKET NUMBER:  2602-A
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (206) 587-0430
CC         TELEFAX:  (206) 233-0644
CC     INFORMATION FOR SEQ ID NO:  6:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  355 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   355 AA; 39008 MW; 711992 CN;

  Query Match             4.8%;  Score 148;  DB 1;  Length 355;
  Best Local Similarity  29.8%;  Pred. No. 3.84e-03;
  Matches    28;  Conservative   19;  Mismatches  40;  Indels   7;  Gaps   6;

Db     27 NGKCKDNEYK-RHHLC--CLSCPPGTYASRLCDSKTNTNTQCTPCASDTFTSRNNHLPAC 83
          :| |:: |:: |   |  |  | ||   |: |      ::|| :|    |   :  :  |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKC 89

Db     84 LSCNGRCDS-NQVETRSCNTTHNRIC-DCAPGYY 115
          :|   |  :|: :  :|::| : || || ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   10
ID   US-08-232-087A-10     STANDARD;     PRT;   154 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 10, Application US/08232087A
XX
CC    Sequence 10, Application US/08232087A
CC    Patent No. 5866372
CC     GENERAL INFORMATION:
CC       APPLICANT:  Stein, Harald
CC       APPLICANT:  D rkop, Horst
CC       APPLICANT:  Latza, Ute
CC       TITLE OF INVENTION:  Lymphoid CD30-Antigen
CC       NUMBER OF SEQUENCES:  11
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Birch, Stewart, Kolasch & Birch, LLP
CC         STREET:  8110 Gatehouse Road, Suite 500 East
CC         CITY:  Falls Church
CC         STATE:  Virginia
CC         COUNTRY:  U.S.A.
CC         ZIP:  22042
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.30
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/232,087A
CC         FILING DATE:  08-SEP-1994
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Murphy Jr., Gerald M.
CC         REGISTRATION NUMBER:  28,977
CC         REFERENCE/DOCKET NUMBER:  756-103P
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (703) 205-8000
CC         TELEFAX:  (703) 205-8050
CC         TELEX:  248345
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CC     INFORMATION FOR SEQ ID NO:  10:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  154 amino acids
CC         TYPE:  amino acid
CC         STRANDEDNESS:  not relevant
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
CC       HYPOTHETICAL:  NO
CC       FRAGMENT TYPE:  internal
CC       FEATURE:
CC         NAME/KEY:  Protein
CC         LOCATION:  1..154
CC         OTHER INFORMATION:  /note= "TNFR1, see Fig. 5"
SQ   SEQUENCE   154 AA; 17350 MW; 115236 CN;

  Query Match             4.7%;  Score 147;  DB 2;  Length 154;
  Best Local Similarity  26.1%;  Pred. No. 4.58e-03;
  Matches    24;  Conservative   20;  Mismatches  44;  Indels   4;  Gaps   4;

Db       2 CPQGKYIHPQNNSICCTKCHKGTYLYNDCP-GPGQDTDCDECESQSFTASENHLRHCLSC 60
           | |  :     | : |  |  |  | ::|  | |:|::|  |  : |   :  :: | :|
Qy      34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPC 92

Db      61 SKCRKEMGQVEISSCTVDRDTVCG-CRKNQYR 91
             |   : : : ::|:   |::|| |    ||
Qy      93 LDCA-VVNRFQKANCSATSDAICGDCLPGFYR 123


RESULT   11
ID   US-08-050-319B-57     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 57, Application US/08050319B
XX
CC    Sequence 57, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  57:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match             4.6%;  Score 143;  DB 1;  Length 167;
  Best Local Similarity  25.2%;  Pred. No. 9.20e-03;
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db      11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
             ::| ||||  :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy       1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db      69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
             ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::||
Qy      59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db     127 CRKNQYR 133
             |   ||
Qy     117 CLPGFYR 123


RESULT   12
ID   US-08-465-982-2     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 2, Application US/08465982
XX
CC    Sequence 2, Application US/08465982
CC    Patent No. 5863786
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/465,982
CC         FILING DATE:
CC         CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319
CC         FILING DATE:  10-May-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match             4.6%;  Score 143;  DB 2;  Length 167;
  Best Local Similarity  25.2%;  Pred. No. 9.20e-03;
```

```
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db     11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
          ::| ||||    :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy      1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db     69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
          ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::||
Qy     59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db    127 CRKNQYR 133
          |    ||
Qy    117 CLPGFYR 123


RESULT   13
ID   US-08-050-319B-2     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 2, Application US/08050319B
XX
CC    Sequence 2, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match             4.6%;  Score 143;  DB 1;  Length 167;
  Best Local Similarity  25.2%;  Pred. No. 9.20e-03;
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db     11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
          ::| ||||    :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy      1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db     69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
          ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::||
Qy     59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db    127 CRKNQYR 133
          |    ||
Qy    117 CLPGFYR 123


RESULT   14
ID   US-08-465-982-57     STANDARD;     PRT;   167 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 57, Application US/08465982
XX
CC    Sequence 57, Application US/08465982
CC    Patent No. 5863786
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/465,982
CC         FILING DATE:
CC         CLASSIFICATION:
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319
CC         FILING DATE:  10-May-1993
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  57:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  167 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   167 AA; 18626 MW; 139513 CN;

  Query Match             4.6%;  Score 143;  DB 2;  Length 167;
  Best Local Similarity  25.2%;  Pred. No. 9.20e-03;
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db     11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
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Qy      1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db     69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
          ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::||
Qy     59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db    127 CRKNQYR 133
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Qy    117 CLPGFYR 123
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RESULT   15
ID   US-08-050-319B-25     STANDARD;     PRT;   455 AA.
XX
AC   xxxxxx
XX
DT
XX
DE   Sequence 25, Application US/08050319B
XX
CC    Sequence 25, Application US/08050319B
CC    Patent No. 5633145
CC     GENERAL INFORMATION:
CC       APPLICANT:  M.Feldmann, P.W. Gray,
CC       APPLICANT:  M.J.C. Turner, F.M Brennan
CC       TITLE OF INVENTION:  Modified human TNFalpha (Tumor
CC       TITLE OF INVENTION:  Necrosis Factor alpha) Receptor
CC       NUMBER OF SEQUENCES:  57
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Reed & Robbins
CC         STREET:  635 Bryant Street
CC         CITY:  Palo Alto
CC         STATE:  California
CC         COUNTRY:  USA
CC         ZIP:  94301
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/050,319B
CC         FILING DATE:  10-May-1993
CC         CLASSIFICATION:  435
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Robbins, Roberta L.
CC         REGISTRATION NUMBER:  33,208
CC         REFERENCE/DOCKET NUMBER:  5150-0030
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (415) 617-8999
CC         TELEFAX:  (415) 327-3231
CC     INFORMATION FOR SEQ ID NO:  25:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  455 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   455 AA; 50579 MW; 1048388 CN;

  Query Match             4.6%;  Score 143;  DB 1;  Length 455;
  Best Local Similarity  25.2%;  Pred. No. 9.20e-03;
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db     11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
          ::| ||||    :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy      1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db     69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
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Qy     59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db    127 CRKNQYR 133
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Qy    117 CLPGFYR 123


Search completed: Tue Apr 18 14:02:57 2000
Job time : 10 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 18 13:57:47 2000; MasPar time 22.57 Seconds
443.989 Million cell updates/sec

Tabular output not generated.

Title: >US-09-490-187-2
Description: (1-423) from US09490187.pep
Perfect Score: 3111
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....AVIHPATQTSLQVRQRLGSL 423

Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
1:geneseqp

Statistics: Mean 34.781; Variance 154.568; scale 0.225

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	3111	100.0	423	1	W93581	Human hAPO4-alpha prot	1.36e-283
2	3066	98.6	423	1	W70387	Amino acid sequence of	3.07e-279
3	3040	97.7	417	1	W98146	Human TRAIN-R.	1.01e-276
4	3007	96.7	417	1	W70386	Amino acid sequence of	1.57e-273
5	2177	70.0	416	1	W93579	Mouse mAPO4-alpha (lon	2.24e-193
6	1368	44.0	214	1	W98145	Mouse TRAIN-R (long fo	1.08e-115
7	1368	44.0	214	1	W93580	Mouse mAPO4-alpha (sho	1.08e-115
8	1193	38.3	150	1	W98148	TRAIN-R short, soluble	5.39e-99
9	1008	32.4	150	1	W93583	Mouse mAPO4-gamma prot	2.06e-81
10	1008	32.4	150	1	W98144	Mouse TRAIN-R (short f	2.06e-81
11	328	10.5	109	1	W93582	Rat rAPO4-alpha protei	2.92e-18
12	248	8.0	30	1	W98147	TRAIN-R secreted form	2.94e-11
13	187	6.0	186	1	R62655	Cowpox virus Pst I/Cla	4.09e-06
14	178	5.7	206	1	W48977	Mouse OX40 extracellul	2.23e-05
15	178	5.7	206	1	R81881	Mouse type-II membrane	2.23e-05
16	178	5.7	438	1	R81882	Plasmid pDC406/OX40/Fc	2.23e-05
17	178	5.7	438	1	W48976	OX40/Fc mutein.	2.23e-05
18	172	5.5	95	1	W93584	Mouse mAPO4-beta prote	6.86e-05
19	159	5.1	176	1	W80254	Amino acid sequence of	7.60e-04
20	151	4.9	159	1	R24083	Truncated TNF-alpha 55	3.27e-03
21	150	4.8	181	1	W26708	Human apoptosis protei	3.92e-03
22	148	4.8	355	1	R85073	Cowpox virus T2-equiva	5.63e-03
23	150	4.8	417	1	W95538	Death domain containin	3.92e-03
24	150	4.8	417	1	W26709	Human apoptosis protei	3.92e-03
25	150	4.8	417	1	W31517	Death domain containin	3.92e-03
26	150	4.8	417	1	W57045	Human apoptosis induci	3.92e-03
27	150	4.8	428	1	W95537	Death domain containin	3.92e-03
28	150	4.8	428	1	W31516	Death domain containin	3.92e-03
29	150	4.8	833	1	W64486	Human DR3 protein.	3.92e-03
30	143	4.6	168	1	R24084	Truncated TNF-alpha 55	1.38e-02
31	143	4.6	199	1	R24080	Truncated TNF-alpha 55	1.38e-02
32	143	4.6	211	1	W89225	Tumour necrosis factor	1.38e-02
33	143	4.6	311	1	W89229	Tumour necrosis factor	1.38e-02
34	143	4.6	366	1	W89228	Tumour necrosis factor	1.38e-02
35	143	4.6	371	1	R07449	Tumour Necrosis Factor	1.38e-02
36	143	4.6	397	1	W89227	Tumour necrosis factor	1.38e-02
37	143	4.6	417	1	W89226	Tumour necrosis factor	1.38e-02
38	143	4.6	420	1	W89224	Tumour necrosis factor	1.38e-02
39	143	4.6	443	1	R51033	Mutant p55 tumour necr	1.38e-02
40	143	4.6	455	1	R11082	Human 55kD TNF-binding	1.38e-02
41	143	4.6	455	1	R42059	Lambda derived TNF-R.	1.38e-02
42	143	4.6	455	1	R51034	Mutant p55 tumour necr	1.38e-02
43	143	4.6	455	1	R10986	30kD TNF inhibitor pre	1.38e-02
44	143	4.6	455	1	R42197	p55 Tumour necrosis fa	1.38e-02
45	143	4.6	455	1	R24000	TNF-alpha 55kD recepto	1.38e-02

ALIGNMENTS

RESULT 1
ID W93581 standard; Protein; 423 AA.
AC W93581;
DT 18-JUN-1999 (first entry)
DE Human hAPO4-alpha protein.
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; APO4-alpha.
OS Homo sapiens.
PN WO9911791-A2.
PD 11-MAR-1999.
PF 04-SEP-1998; U18393.
PR 05-SEP-1997; US-924634.
PA (UNIW) UNIV WASHINGTON.
PI Chaudhary PM;
DR WPI; 99-205191/17.
DR N-PSDB; X23415.
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
PS Claim 1; Fig 7C; 156pp; English.
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
SQ Sequence 423 AA;

Query Match 100.0%; Score 3111; DB 1; Length 423;

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  Best Local Similarity 100.0%;  Pred. No. 1.36e-283;
  Matches   423;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
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Qy      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
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Qy    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db    181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETELSCFDRPQLHEYAHRACCQCRRD 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETELSCFDRPQLHEYAHRACCQCRRD 240

Db    241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db    301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Db    361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQVRQRL 420
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Qy    361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQVRQRL 420

Db    421 GSL 423
          |||
Qy    421 GSL 423


RESULT    2
ID   W70387 standard; Protein; 423 AA.
AC   W70387;
DT   02-DEC-1998  (first entry)
DE   Amino acid sequence of human beta-OAF065.
KW   Human; beta-OAF065; stroma cell; antibody; inflammatory;
KW   cytokine-mediated disease; rheumatism; ulcerative colitis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Misc_difference 223
FT                   /note= "encoded by AGA"
FT   Misc_difference 224
FT                   /note= "encoded by CCT"
PN   WO9838304-A1.
PD   03-SEP-1998.
PF   26-FEB-1998; J00799.
PR   27-FEB-1997; JP-043143.
PA   (ONOY ) ONO PHARM CO LTD.
PI   Fukushima D, Konishi M, Tada H;
DR   WPI; 98-481205/41.
DR   N-PSDB; V33362.
PT   Membrane polypeptide expressed by human stroma cells, and antibodies
PT   recognising it - for treatment of inflammatory and other
PT   cytokine-mediated diseases.
PS   Disclosure; Pages 37-49; 54pp; Japanese.
CC   This is the amino acid sequence of the human beta-OAF065, used in
CC   the method of the invention.  The process involves the use of peptides
CC   expressed by stroma cells, and its antibodies are used for in the
CC   prevention and treatment of inflammatory and other cytokine-mediated
CC   diseases such as rheumatism, ulcerative colitis.
SQ   Sequence   423 AA;

  Query Match           98.6%;  Score 3066;  DB 1;  Length 423;
  Best Local Similarity  98.1%;  Pred. No. 3.07e-279;
  Matches   415;  Conservative    5;  Mismatches   3;  Indels   0;  Gaps   0;

Db      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCETGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db     61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db    181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCLDPRQLHEYAHRACCQCRRD 240
          ||||||||||||||||||||||||||||||||||| :||||:|  ||||||||||||||||
Qy    181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETELSCFDRPQLHEYAHRACCQCRRD 240

Db    241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
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Qy    241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db    301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
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Qy    301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Db    361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQVRQRL 420
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Qy    361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQVRQRL 420

Db    421 GSL 423
          |||
Qy    421 GSL 423


RESULT    3
ID   W98146 standard; Protein; 417 AA.
AC   W98146;
DT   05-JUL-1999  (first entry)
DE   Human TRAIN-R.
KW   TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Peptide         1. .21
FT                   /note= "signal peptide"
FT   Protein         22. .417
FT                   /note= "mature protein"
FT   Domain          26. .173
FT                   /note= "extracellular domain"
FT   Domain          174. .190
FT                   /note= "transmembrane domain"
FT   Domain          191. .417
FT                   /note= "cytoplasmic domain"
PN   WO9913078-A1.
PD   18-MAR-1999.
PF   11-SEP-1998; U19030.
PR   06-MAY-1998; US-084422.
PR   12-SEP-1997; US-058631.
PA   (BIOJ ) BIOGEN INC.
PI   Hession C, Tschopp J;
DR   WPI; 99-229238/19.
DR   N-PSDB; X24978.
PT   New cysteine-rich tumor necrosis factor receptor
PS   Claim 2; Page 26; 30pp; English.
CC   The present sequence is a novel human cysteine-rich tumour
CC   necrosis factor receptor family member termed TRAIN-R that is
CC   expressed at low levels in every tissue and cell line tested thus
CC   far, with higher expression detected in heart, prostate, ovary,
CC   testis, peripheral blood lymphocytes, thyroid and adrenal gland.
CC   Cell death can be induced by administering an agent capable of
CC   inhibiting the binding of TRAIN-R to its ligand.  A claimed method
CC   of treating, or reducing, the advancement, severity or effects of
CC   an immunological disease in a mammal comprises administering a
CC   pharmaceutical composition which comprises a TRAIN-R blocking agent,
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CC   e.g. soluble TRAIN-R.  TRAIN-R can be fused to an immunoglobulin to
CC   produce a fusion protein which may be targeted to various sites.
CC   It can be used in binding assays, and to identify antagonists and
CC   agonists.  Anti-TRAIN-R antibodies can be used to reduce the
CC   severity of an immune response or to treat cancer.  TRAIN-R
CC   blocking agents can also be used to reduce the severity or effects
CC   of an immunological disease (all claimed).
SQ   Sequence   417 AA;

  Query Match           97.7%;  Score 3040;  DB 1;  Length 417;
  Best Local Similarity  99.3%;  Pred. No. 1.01e-276;
  Matches   412;  Conservative    2;  Mismatches   1;  Indels   0;  Gaps   0;

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Qy       1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db      61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
Qy      61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db     181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD 240
Qy     181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETELSCFDRPQLHEYAHRACCQCRRD 240

Db     241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy     241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db     301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Qy     301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Db     361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQ 415
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RESULT    4
ID   W70386 standard; Protein; 417 AA.
AC   W70386;
DT   02-DEC-1998  (first entry)
DE   Amino acid sequence of human alpha-OAF065.
KW   Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW   cytokine-mediated disease; rheumatism; ulcerative colitis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   Misc_difference 223
FT                   /note= "encoded by AGA""
FT   Misc_difference 224
FT                   /note= "encoded by CCT"
PN   WO9838304-A1.
PD   03-SEP-1998.
PF   26-FEB-1998; J00799.
PR   27-FEB-1997; JP-043143.
PA   (ONOY ) ONO PHARM CO LTD.
PI   Fukushima D, Konishi M, Tada H;
DR   WPI; 98-481205/41.
DR   N-PSDB; V33361.
PT   Membrane polypeptide expressed by human stroma cells, and antibodies
PT   recognising it - for treatment of inflammatory and other
PT   cytokine-mediated diseases.
PS   Claim 1; Pages 28-30; 54pp; Japanese.
CC   This is the amino acid sequence of the human alpha-OAF065, used in
CC   the method of the invention.  The process involves the use of peptides
CC   expressed by stroma cells, and its antibodies are used for in the
CC   prevention and treatment of inflammatory and other cytokine-mediated
CC   diseases such as rheumatism, ulcerative colitis.
SQ   Sequence   417 AA;

  Query Match           96.7%;  Score 3007;  DB 1;  Length 417;
  Best Local Similarity  98.1%;  Pred. No. 1.57e-273;
  Matches   407;  Conservative    5;  Mismatches   3;  Indels   0;  Gaps   0;

Db       1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCETGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
Qy       1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db      61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
Qy      61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Qy     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db     181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCLDPRQLHEYAHRACCQCRRD 240
Qy     181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETELSCFDRPQLHEYAHRACCQCRRD 240

Db     241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Qy     241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db     301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
Qy     301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Db     361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAIIHPATQTSLQ 415
Qy     361 PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQ 415


RESULT    5
ID   W93579 standard; Protein; 416 AA.
AC   W93579;
DT   18-JUN-1999  (first entry)
DE   Mouse mAPO4-alpha (long) protein.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; mAPO4-alpha.
OS   Mus sp.
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   N-PSDB; X23413.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Claim I; Fig 7A; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
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CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
SQ   Sequence   416 AA;

  Query Match           70.0%;  Score 2177;  DB 1;  Length 416;
  Best Local Similarity  70.5%;  Pred. No. 2.24e-193;
  Matches   294;  Conservative   63;  Mismatches  55;  Indels   5;  Gaps   5;

Db       1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60
           ||||||  :   :|: :::|  |:|||:||:||||||||:|||||||  |:||||||||||
Qy       1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db      61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120
           |||||||||||||:|| ||||||||||||||| |||:|||||:|||| ||||:|||||||
Qy      61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
           ||||||||||||||||||||||||||||:||||||||:|| ||||||||||||||||||
Qy     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db     181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDQPRLRHCAHRACCQYHRD 240
           |||||||||||||||||||||||||||||| :|||||:|:|:  |||||||  :||
Qy     181 VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNETELSCFDRPQLHEYAHRACCQCRRD 240

Db     241 SAPMYGPVHLIPSLCCEEARSSARAVLGCGLRSPTTLQERNPASVGNTMPAFFGSVSRSI 300
           |    |||:|:||:|||| |:  | ||||::|:::|| ||::: |: :|:||||:::||
Qy     241 SVQTCGPVRLLPSMCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db     301 CAEFSDAWPLMQNPLGGDS-SLCDSYPELTGEDTNSLNPENESTASLDSSGGQDLAGTA- 358
           |:||||||||||:|||: |:|||||||||| :||||| ||::||||:::||| | |
Qy     301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360

Db     359 ALES-SGNVSESTDSPRHGDTGTVWEQTLAQDAQRTPSQGGWEDRENLNLAMPTAFQ 414
           :::| | | : :|| :|  :|  | | : :|||    ||   |    :: |  |:::|
Qy     361 PVQSHSENFTAATDLSRYNNT-LV-ESASTQDALTMRSQLDQESGAVIHPATQTSLQ 415


RESULT    6
ID   W98145 standard; Protein; 214 AA.
AC   W98145;
DT   05-JUL-1999  (first entry)
DE   Mouse TRAIN-R (long form).
KW   TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic.
OS   Mus musculus.
PN   WO9913078-A1.
PD   18-MAR-1999.
PF   11-SEP-1998; U19030.
PR   06-MAY-1998; US-084422.
PR   12-SEP-1997; US-058631.
PA   (BIOJ ) BIOGEN INC.
PI   Hession C, Tschopp J;
DR   WPI; 99-229238/19.
DR   N-PSDB; X24977.
PT   New cysteine-rich tumor necrosis factor receptor
PS   Claim 2; Page 26; 30pp; English.
CC   The present sequence is a novel murine cysteine-rich tumour
CC   necrosis factor receptor family member termed TRAIN-R (long form).
CC   TRAIN-R is expressed at high levels in murine brain and lung, and
CC   at lower levels in liver, skeletal muscle and kidney.  Cell death
CC   can be induced by administering an agent capable of inhibiting the
CC   binding of TRAIN-R to its ligand.  A claimed method of treating, or
CC   reducing, the advancement, severity or effects of an immunological
CC   disease in a mammal comprises administering a pharmaceutical
CC   composition which comprises a TRAIN-R blocking agent, e.g. soluble
CC   TRAIN-R (see W98144).  TRAIN-R can be fused to an immunoglobulin
CC   molecule to produce a fusion protein which may be targeted to
CC   various sites.  It can be used in binding assays, and to identify
CC   antagonists and agonists.  Anti-TRAIN receptor antibodies can be
CC   used to reduce the severity of an immune response or to treat cancer.
CC   TRAIN-R blocking agents can be used to reduce the severity or effects
CC   of an immunological disease (all claimed).
SQ   Sequence   214 AA;

  Query Match           44.0%;  Score 1368;  DB 1;  Length 214;
  Best Local Similarity  85.2%;  Pred. No. 1.08e-115;
  Matches   173;  Conservative   17;  Mismatches  13;  Indels   0;  Gaps   0;

Db       1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60
           ||||||  :   :|: :::|  |:|||:||:||||||||:|||||||  |:||||||||||
Qy       1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db      61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120
           |||||||||||||:|| ||||||||||||||| |||:|||||:|||| ||||:|||||||
Qy      61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
           ||||||||||||||||||||||||||||:||||||||:|| ||||||||||||||||||
Qy     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db     181 VLLALLILCVIYCKRQFMEKKPS 203
           |||||||||||||||||||||||
Qy     181 VLLALLILCVIYCKRQFMEKKPS 203


RESULT    7
ID   W93580 standard; Protein; 214 AA.
AC   W93580;
DT   18-JUN-1999  (first entry)
DE   Mouse mAPO4-alpha (short) protein.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; mAPO4-alpha.
OS   Mus sp.
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   N-PSDB; X23414.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Claim 1; Fig 7B; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents; useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
SQ   Sequence   214 AA;

  Query Match           44.0%;  Score 1368;  DB 1;  Length 214;
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```
  Best Local Similarity  85.2%;  Pred. No. 1.08e-115;
  Matches   173;  Conservative   17;  Mismatches  13;  Indels   0;  Gaps   0;

Db      1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60
          ||||||  :   :|: :::|  |:|||:||:||||||||:|||||| |:||||||||||
Qy      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db     61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120
          |||||||||||||:|| |||||||||||||| |||:|||||:|||| ||||:|||||||
Qy     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCTSKVNLVKISSTVSSPRDTALAAVICSALAT 180
          ||||||||||||||||||||||||||||||:||||||||:|| ||||||||||||||||
Qy    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

Db    181 VLLALLILCVIYCKRQFMEKKPS 203
          |||||||||||||||||||||||
Qy    181 VLLALLILCVIYCKRQFMEKKPS 203


RESULT    8
ID   W98148 standard; Peptide; 150 AA.
AC   W98148;
DT   05-JUL-1999  (first entry)
DE   TRAIN-R short, soluble form.
KW   TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic.
OS   Homo sapiens.
PN   WO9913078-A1.
PD   18-MAR-1999.
PF   11-SEP-1998; U19030.
PR   06-MAY-1998; US-084422.
PR   12-SEP-1997; US-058631.
PA   (BIOJ ) BIOGEN INC.
PI   Hession C, Tschopp J;
DR   WPI; 99-229238/19.
PT   New cysteine-rich tumor necrosis factor receptor
PS   Disclosure; Page 28; 30pp; English.
CC   The present sequence comprises the putative short, secreted soluble
CC   form of a novel human cysteine-rich tumour necrosis factor receptor
CC   family member termed TRAIN-R.  The sequence was produced from a
CC   30-amino acid peptide (see W98147) encoded by a cloned exon
CC   sequence (see X24979) and by comparison to the murine TRAIN-R
CC   short form (see W98144).  The human soluble TRAIN-R protein is
CC   expected to inhibit signalling by full-length human TRAIN-R (see
CC   W98146).  Human TRAIN-R is expressed at low levels in every tissue
CC   and cell line tested thus far, with higher expression detected in
CC   heart, prostate, ovary, testis, peripheral blood lymphocytes,
CC   thyroid and adrenal gland.  Cell death can be induced by
CC   administering an agent capable of inhibiting the binding of TRAIN-R
CC   to its ligand.  A claimed method of treating, or reducing, the
CC   advancement, severity or effects of an immunological disease in a
CC   mammal comprises administering a pharmaceutical composition which
CC   comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R.  TRAIN-R
CC   can be fused to an immunoglobulin to produce a fusion protein which
CC   may be targeted to various sites.  It can be used in binding assays,
CC   and to identify antagonists and agonists.  Anti-TRAIN-R antibodies
CC   can be used to reduce the severity of an immune response or to treat
CC   cancer.  TRAIN-R blocking agents can also be used to reduce the
CC   severity or effects of an immunological disease (all claimed).
SQ   Sequence   150 AA;

  Query Match           38.3%;  Score 1193;  DB 1;  Length 150;
  Best Local Similarity  99.3%;  Pred. No. 5.39e-99;
  Matches   148;  Conservative    1;  Mismatches   0;  Indels   0;  Gaps   0;

Db      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db     61 ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120
          |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Qy     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149
          |||||||||||||||||||||||||||||
Qy    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149


RESULT    9
ID   W93583 standard; Protein; 150 AA.
AC   W93583;
DT   18-JUN-1999  (first entry)
DE   Mouse mAPO4-gamma protein.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; APO4-gamma.
OS   Mus sp.
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   N-PSDB; X23417.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Disclosure; Fig 7E; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
SQ   Sequence   150 AA;

  Query Match           32.4%;  Score 1008;  DB 1;  Length 150;
  Best Local Similarity  81.9%;  Pred. No. 2.06e-81;
  Matches   122;  Conservative   15;  Mismatches  12;  Indels   0;  Gaps   0;

Db      1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60
          ||||||  :   :|: :::|  |:|||:||:||||||||:|||||| |:||||||||||
Qy      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db     61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120
          |||||||||||||:|| |||||||||||||| |||:|||||:|||| ||||:|||||||
Qy     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149
          |||||||||:||||||||||||||||||||
Qy    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149


RESULT   10
ID   W98144 standard; Protein; 150 AA.
AC   W98144;
```

DT 05-JUL-1999 (first entry)
DE Mouse TRAIN-R (short form).
KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic.
OS Mus musculus.
PN WO9913078-A1.
PD 18-MAR-1999.
PF 11-SEP-1998; U19030.
PR 06-MAY-1998; US-084422.
PR 12-SEP-1997; US-058631.
PA (BIOJ) BIOGEN INC.
PI Hession C, Tschopp J;
DR WPI; 99-229238/19.
DR N-PSDB; X24976.
PT New cysteine-rich tumor necrosis factor receptor
PS Claim 2; Page 26; 30pp; English.
CC The present sequence is a novel murine cysteine-rich tumour
CC necrosis factor receptor family member termed TRAIN-R (short form).
CC This putative natural soluble form of murine TRAIN-R may inhibit
CC signalling by the full-length TRAIN-R (see W98145). Murine
CC TRAIN-R is expressed at high levels in brain and lung, and at
CC lower levels in liver, skeletal muscle and kidney. Cell death
CC can be induced by administering an agent capable of inhibiting the
CC binding of TRAIN-R to its ligand. A claimed method of treating, or
CC reducing, the advancement, severity or effects of an immunological
CC disease in a mammal comprises administering a pharmaceutical
CC composition which comprises a TRAIN-R blocking agent, e.g. soluble
CC TRAIN-R. TRAIN-R can be fused to an immunoglobulin molecule to
CC produce a fusion protein which may be targeted to various sites.
CC It can be used in binding assays, and to identify antagonists and
CC agonists. Anti-TRAIN receptor antibodies can be used to reduce the
CC severity of an immune response or to treat cancer. TRAIN-R
CC blocking agents can be used to reduce the severity or effects of an
CC immunological disease (all claimed).
SQ Sequence 150 AA;

Query Match 32.4%; Score 1008; DB 1; Length 150;
Best Local Similarity 81.9%; Pred. No. 2.06e-81;
Matches 122; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

```
Db      1 MALKVLPLHRTVLFAAILFLLHLACKVSCETGDCRQQEFKDRSGNCVLCKQCGPGMELSK 60
          ||||||  :   :|: :::|  |:|||:||:||||||||:||||||| |:||||||||||
Qy      1 MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK 60

Db     61 ECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNRFQRANCSHTSDAVCGDCLPG 120
          |||||||||||||:|| ||||||||||||||| |||:|||||:|||| ||||:|||||||
Qy     61 ECGFGYGEDAQCVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120

Db    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149
          |||||||||||||||||||||||||||||
Qy    121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149
```

RESULT 11
ID W93582 standard; Protein; 109 AA.
AC W93582;
DT 18-JUN-1999 (first entry)
DE Rat rAPO4-alpha protein.
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; rat; APO4-alpha.
OS Rattus sp.
PN WO9911791-A2.
PD 11-MAR-1999.
PF 04-SEP-1998; U18393.
PR 05-SEP-1997; US-924634.
PA (UNIW) UNIV WASHINGTON.
PI Chaudhary PM;
DR WPI; 99-205191/17.
DR N-PSDB; X23416.
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
PS Claim 1; Fig 7D; 156pp; English.
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
SQ Sequence 109 AA;

Query Match 10.5%; Score 328; DB 1; Length 109;
Best Local Similarity 54.5%; Pred. No. 2.92e-18;
Matches 60; Conservative 22; Mismatches 23; Indels 5; Gaps 5;

```
Db      1 WPLMQNPLGGDS-SLCDSYPELTGEDINSLNPENESSTSVDSNGGQDLAGAAAP-DS-SG 57
          |||||||:|||: |:|||||||||||||:||||| |||||:|||::||| |:| | :| |
Qy    308 WPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAVPVQSHSE 367

Db     58 DFQENTDSPFYGDADTVWEQTLAQDAQRTPSREGWEASENLNLATSTAFQ 107
          :|   || :|| ::  | | : :|||    |:   |::  :: || |::|
Qy    368 NFTAATDLSRYNNT-LV-ESASTQDALTMRSQLDQESGAVIHPATQTSLQ 415
```

RESULT 12
ID W98147 standard; Peptide; 30 AA.
AC W98147;
DT 05-JUL-1999 (first entry)
DE TRAIN-R secreted form C-terminal peptide.
KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic.
OS Homo sapiens.
PN WO9913078-A1.
PD 18-MAR-1999.
PF 11-SEP-1998; U19030.
PR 06-MAY-1998; US-084422.
PR 12-SEP-1997; US-058631.
PA (BIOJ) BIOGEN INC.
PI Hession C, Tschopp J;
DR WPI; 99-229238/19.
DR N-PSDB; X24979.
PT New cysteine-rich tumor necrosis factor receptor
PS Claim 2; Page 26; 30pp; English.
CC The present sequence comprises the C-terminal 30 amino acids of a
CC soluble form of a novel human cysteine-rich tumour necrosis factor
CC receptor family member termed TRAIN-R. The 30-amino acid peptide
CC is identical to amino acids 121-149 of the composite human TRAIN-R
CC protein sequence given in W98146 and to amino acids 121-150 of the
CC C-terminus of murine TRAIN-R short form (secreted protein, see
CC W98144). The amino acid sequence of the entire short secreted form
CC of human TRAIN-R was deduced (see W98148) from the cloned exon
CC sequence and by comparison to the mouse short form. The human
CC soluble protein is expected to inhibit signalling by the full-length
CC TRAIN-R. Human TRAIN-R is expressed at low levels in every tissue
CC and cell line tested thus far, with higher expression detected in
CC heart, prostate, ovary, testis, peripheral blood lymphocytes,

```
CC   thyroid and adrenal gland.  Cell death can be induced by
CC   administering an agent capable of inhibiting the binding of TRAIN-R
CC   to its ligand.  A claimed method of treating, or reducing, the
CC   advancement, severity or effects of an immunological disease in a
CC   mammal comprises administering a pharmaceutical composition which
CC   comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R.  TRAIN-R
CC   can be fused to an immunoglobulin to produce a fusion protein which
CC   may be targeted to various sites.  It can be used in binding assays,
CC   and to identify antagonists and agonists.  Anti-TRAIN-R antibodies
CC   can be used to reduce the severity of an immune response or to treat
CC   cancer.  TRAIN-R blocking agents can also be used to reduce the
CC   severity or effects of an immunological disease (all claimed).
SQ   Sequence   30 AA;

  Query Match           8.0%;  Score 248;  DB 1;  Length 30;
  Best Local Similarity 100.0%;  Pred. No. 2.94e-11;
  Matches   29;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Db       1 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 29
           |||||||||||||||||||||||||||||
Qy     121 FYRKTKLVGFQDMECVPCGDPPPPYEPHC 149


RESULT   13
ID   R62655 standard; Protein; 186 AA.
AC   R62655;
DT   30-JUN-1995  (first entry)
DE   Cowpox virus Pst I/Cla I fragment viral protein .
KW   Cowpox virus fragment Pat I/Cla I; cytokine antagonist;
KW   tumour necrosis factor; immune response regulation.
OS   Cowpox virus.
PN   US5359039-A.
PD   25-OCT-1994.
PF   09-JUL-1993; 089458.
PR   09-JUL-1993; US-089458.
PA   (IMMV ) IMMUNEX CORP.
PI   Goodwin RG,  Smith CA;
DR   WPI; 94-341063/42.
DR   N-PSDB; Q72995.
PT   Isolated viral proteins capable of binding TNF -  therefore
PT   functioning as TNF and cytokine antagonists
PS   Claim 1; Columns 21-22; 13pp; English.
CC   Q72995 encodes R62655 a viral protein from the Pst I/Cla I
CC   fragment of the cowpox virus, which binds cytokines and tumour
CC   necrosis factor (TNF). The viral protein can be used to regulate
CC   immune response as part of a therapeutic composition, it can also
CC   be used as an antagonist of TNF.
SQ   Sequence   186 AA;

  Query Match           6.0%;  Score 187;  DB 1;  Length 186;
  Best Local Similarity 30.0%;  Pred. No. 4.09e-06;
  Matches   33;  Conservative   28;  Mismatches  40;  Indels   9;  Gaps   9;

Db      34 NGSCDDGEYLDKTHN-QCCNRCPPG-EFAKIRCS-G-SDNTKCERCPPHTYTTVPNYSNG 89
           :| | : |: |:: |   ||:| || |::|  |: | :::: |  |  | :     : :
Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKE-CGFGYGEDAQCVACRLHRFKEDWGFQK- 88

Db      90 CHQCRKCPT-GSFDKVKCTGTQNSKCS-CLPGWFCATDSSKTEDCRDCIP 137
           |  |  |:    |:| :|::| :: |: |||| :  |     :|  :|:|
Qy      89 CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQD-MECVP 137


RESULT   14
ID   W48977 standard; Protein; 206 AA.
AC   W48977;
DT   25-SEP-1998  (first entry)
DE   Mouse OX40 extracellular domain.
KW   OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;
KW   OX40/Fc.
OS   Mus sp.
PN   US5783665-A.
PD   21-JUL-1998.
PF   22-JUN-1995; 494574.
PR   23-JUL-1993; US-097827.
PR   22-JUN-1995; US-494574.
PA   (IMMV ) IMMUNEX CORP.
PI   Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
DR   WPI; 98-427099/36.
DR   N-PSDB; V32640.
PT   Purified polypeptide OX-40 ligands - for co:stimulation of T-cell
PT   production and binding assays for OX-40 and homologues
PS   Example 1; Col 33-34; 26pp; English.
CC   The present sequence represents the mouse OX40 extracellular domain
CC   The extracellular domain of OX40 is its ligand binding domain.  The
CC   cDNA (V32640) encoding OX40 extracellular domain was used in the
CC   construction of the chimeric OX40/Fc cDNA (V32640).  The invention
CC   claims for a murine OX40-L cytokine (W48975) that binds to the OX40
CC   murine T cell antigen.  The OX40-L protein is claimed to be useful
CC   for co-stimulation of T-cell production and in binding assays for
CC   detecting OX40 or its homologues.  The OX40-L protein is also claimed
CC   to generate a TH-2 immune response.
SQ   Sequence   206 AA;

  Query Match           5.7%;  Score 178;  DB 1;  Length 206;
  Best Local Similarity 27.8%;  Pred. No. 2.23e-05;
  Matches   49;  Conservative   36;  Mismatches  77;  Indels  14;  Gaps  11;

Db       9 TALLLG-LTLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVNRCD--HTRDTLCHP 62
           | |:||| |:  ||    :|  : :   : :|  | :| ||  : : |      |: | :
Qy      15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db      63 CETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLG 120
           |    ::|   :: || | :|   :  : | ||::| |::|  | ||   :    |:
Qy      75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQ-D 132

Db     121 VDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CED-RSLLATLL 174
           ::|||  |  :|  :  | :  |    :  :  |   :| || |    ::| :||
Qy     133 MECVPC--GDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALATVLLALL 186


RESULT   15
ID   R81881 standard; Protein; 206 AA.
AC   R81881;
DT   08-JUL-1996  (first entry)
DE   Mouse type-II membrane polypeptide OX40 extracellular domain.
KW   OX40; OX40-L; cytokine; cell surface molecule;
KW   membrane glycoprotein.
OS   Mus musculus.
PN   US5457035-A.
PD   10-OCT-1995.
PF   23-JUL-1993; 097827.
PR   23-JUL-1993; US-097827.
PA   (IMMV ) IMMUNEX CORP.
PI   Baum PR,  Fanslow WC,  Gayle RB,  Goodwin RG;
DR   WPI; 95-357992/46.
DR   N-PSDB; T00826.
PT   New isolated DNA encoding the OX40 ligand polypeptide - also vectors
PT   and host cells. used to produce recombinant ligand used in e.g.
PT   prim. T cell culture, to modulate immune response etc.
PS   Example 1; Column 33-34; 26pp; English.
CC   This sequence encodes the extracellular domain of OX40, a membrane
CC   glycoprotein present on the CD4 positive subset of activated T
CC   cells.
SQ   Sequence   206 AA;

  Query Match           5.7%;  Score 178;  DB 1;  Length 206;
  Best Local Similarity 27.8%;  Pred. No. 2.23e-05;
  Matches   49;  Conservative   36;  Mismatches  77;  Indels  14;  Gaps  11;

Db       9 TALLLG-LTLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVNRCD--HTRDTLCHP 62
           | |:||| |:  ||    :|  : :   : :|  | :| ||  : : |      |: | :
Qy      15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db      63 CETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLG 120
           |    ::|   :: || | :|   :  : | ||::| |::|  | ||   :    |:
Qy      75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQ-D 132
```

```
Db     121 VDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CED-RSLLATLL 174
           ::|||| | :| : | : |   : : |  :| || |   ::| :||
Qy     133 MECVPC--GDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALATVLLALL 186
```

Search completed: Tue Apr 18 13:58:13 2000
Job time : 26 secs.

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 23, 2000, 01:27:45 ; Search time 463.49 Seconds
(without alignments)
12129.633 Million cell updates/sec

Title: US-09-490-187-1
Perfect score: 1489
Sequence: 1 ggacctgcagcctcccaggt.....gtatttttttaaaaaacttt 1489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 1887831982 residues

Total number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
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19: em_est19:*
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23: gb_est4:*
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101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	454	30.5	454	26	W56629	W56629 zd16e11.r1
2	272.2	18.3	282	61	AL036000	AL036000 DKFZp564K

	3	214	14.4	401	27	AA003356	AA003356 mg49g01.r
	4	185	12.4	358	27	AA036247	AA036247 mi74a03.r
	5	153.4	10.3	643	104	AQ563354	AQ563354 HS_5335_B
	6	124.4	8.4	275	59	AV111112	AV111112 AV111112
	7	122.6	8.2	646	104	AQ544065	AQ544065 RPCI-11-3
	8	116	7.8	404	34	AA495217	AA495217 fa04d10.r
c	9	112.2	7.5	450	104	AQ514075	AQ514075 HS_5184_A
	10	78.6	5.3	381	48	AI551729	AI551729 vf11e02.y
	11	61.8	4.2	485	64	AL120773	AL120773 DKFZp762C
c	12	59	4.0	405	99	AQ173919	AQ173919 HS_3204_A
c	13	43.4	2.9	1101	79	CNS00LPM	AL068516 Drosophil
c	14	42.6	2.9	443	38	AA759377	AA759377 ah54a10.s
c	15	42.4	2.8	806	79	CNS009YZ	AL054514 Drosophil
c	16	41.4	2.8	551	38	AA814296	AA814296 nz07d08.s
c	17	41.2	2.8	1101	79	CNS00K81	AL077341 Drosophil
	18	40.6	2.7	313	50	AI668861	AI668861 wb82b04.x
	19	40.6	2.7	1101	79	CNS00BEU	AL056987 Drosophil
	20	40.4	2.7	1201	80	CNS0162K	AL106214 Drosophil
	21	40.2	2.7	697	80	CNS018M5	AL109511 Drosophil
	22	40.2	2.7	778	38	AA748343	AA748343 oa55b03.s
c	23	40	2.7	209	74	AW196030	AW196030 xl86f10.x
	24	40	2.7	948	80	CNS0159T	AL105179 Drosophil
c	25	39.8	2.7	1101	79	CNS00LJT	AL068307 Drosophil
c	26	39.6	2.7	242	73	AW168427	AW168427 xi83c09.x
c	27	39.6	2.7	494	74	AW194174	AW194174 xm07c04.x
	28	39.6	2.7	1009	79	CNS00587	AL057153 Drosophil
c	29	39.6	2.7	1047	80	CNS0164P	AL106291 Drosophil
c	30	39.4	2.6	397	39	AA860208	AA860208 ak48c10.s
c	31	39.4	2.6	465	26	W47341	W47341 zc34h02.s1
c	32	39.4	2.6	962	79	CNS007P9	AL067452 Drosophil
	33	39.4	2.6	1101	79	CNS00M7T	AL079245 Drosophil
	34	39.2	2.6	418	63	AI963611	AI963611 wr65e05.x
c	35	39.2	2.6	540	48	AI610254	AI610254 tp14b09.x
c	36	39	2.6	207	44	AU037991	AU037991 AU037991
c	37	39	2.6	407	26	W32428	W32428 zc05c12.s1
	38	39	2.6	448	81	B51424	B51424 CIT978SK-18
c	39	39	2.6	559	29	AA161105	AA161105 zo58c05.s
c	40	39	2.6	964	80	CNS017VX	AL108567 Drosophil
c	41	39	2.6	1101	79	CNS00Z2U	AL097152 Drosophil
	42	38.8	2.6	925	79	CNS0091P	AL053013 Drosophil
	43	38.8	2.6	1101	79	CNS00AY1	AL056483 Drosophil
c	44	38.6	2.6	539	44	AI258473	AI258473 LP01680.5
c	45	38.6	2.6	594	43	AU034113	AU034113 AU034113

ALIGNMENTS

```
RESULT   1
W56629
LOCUS       W56629          454 bp    mRNA            EST       15-OCT-1996
DEFINITION  zd16e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
            IMAGE:340844 5', mRNA sequence.
ACCESSION   W56629
VERSION     W56629.1  GI:1358487
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:785895.
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1373   Std Error: 0.00
            Seq primer: mob.REGA+ET.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Homo sapiens"
                     /db_xref="GDB:1266219"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:340844"
                     /clone_lib="Soares_fetal_heart_NbHH19W"
                     /sex="unknown"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by
                     M.Fatima Bonaldo. This library was constructed from the
                     same fetus as the fetal lung library, Soares fetal lung
                     NbHL19W."
BASE COUNT      132 a     96 c     88 g    138 t
ORIGIN


  Query Match           30.5%;  Score 454;  DB 26;  Length 454;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-109;
  Matches  454;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1036 ctcttatcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctc 1095
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Db      1 CTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAATCCAGAACTTGAAAGCTC 60

Qy   1096 aacgtctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtc 1155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTC 120

Qy   1156 tcattctgaaaactttacagcagctactgatttatctagatataacaacacactggtaga 1215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAACACACTGGTAGA 180

Qy   1216 atcagcatcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgc 1275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGC 240

Qy   1276 tgtcatccacccagccactcagacgtccctccaggtaaggcagcgactgggttccctgtg 1335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGTAAGGCAGCGACTGGGTTCCCTGTG 300

Qy   1336 aacacagcactgacttacagtagatcagaactctgttcccagcataagatttgggggaac 1395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AACACAGCACTGACTTACAGTAGATCAGAACTCTGTTCCCAGCATAAGATTTGGGGGAAC 360

Qy   1396 ctggatgagttttttttttttgcatctttaataatttcttatatgttgtagagtatgtttt 1455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTGGATGAGTTTTTTTTTTTGCATCTTTAATAATTTCTTATATGTTGTAGAGTATGTTTT 420

Qy   1456 aaaataaatttcaagtatttttttaaaaaactt 1489
          ||||||||||||||||||||||||||||||||
Db    421 AAAATAAATTTCAAGTATTTTTTTAAAAAACTTT 454


RESULT   2
AL036000
LOCUS       AL036000        282 bp    mRNA            EST       27-SEP-1999
DEFINITION  DKFZp564K1022_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
```

```
          DKFZp564K1022 5', mRNA sequence.
ACCESSION AL036000
VERSION   AL036000.1  GI:5405629
KEYWORDS  EST.
SOURCE    human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1  (bases 1 to 282)
  AUTHORS   Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     EST (Wambutt, et al.)
  JOURNAL   Unpublished (1999)
COMMENT   On Jun 22, 1998 this sequence version replaced gi:3246658.
          Contact: Wambutt R
          MIPS
          Am Klopferspitz 18a D-82152 Martinsried, Germany
          This is the 5' sequence of the clone insert
          Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
          Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
          sequenced by AGOWA within the cDNA sequencing consortium of the
          German Genome Project.
          s1 sequence also available.
          This clone is available at the RZPD in Berlin.
          Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
          Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES             Location/Qualifiers
     source          1. .282
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp564K1022"
                     /clone_lib="564 (synonym: hfbr2)"
                     /tissue_type="brain"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
BASE COUNT       57 a     85 c     75 g     63 t      2 others
ORIGIN
```

```
  Query Match             18.3%;  Score 272.2;  DB 61;  Length 282;
  Best Local Similarity   98.2%;  Pred. No. 2.4e-61;
  Matches  274;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    429 ataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctc 488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3 ATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTC 62

Qy    489 ctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacgg 548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 CTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGG 122

Qy    549 cctccagcccacgggacacggcgctggctgccgttatctgcagcgctctggccaccgtcc 608
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    123 CCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCANCGCTCTGGCCACCGTCC 182

Qy    609 tgctggccctgctcatcctctgtgtcatctattgtaagagacagtttatggaaaagaaac 668
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    183 TGCTGGCCCTGCTCATCCTCTGTGTCATCTATTGTAAGAGACAGTTTATGGAGAAGAAAC 242

Qy    669 ccagctggtctctgcggtcacaggacattcagtacaacg 707
          ||||||||||||||||| || ||||||||||| |||
Db    243 CCAGCTGGTCTCTGCGGTCGCANGACATTCAGTACTACG 281
```

```
RESULT   3
AA003356
LOCUS       AA003356      401 bp    mRNA            EST       19-JUL-1996
DEFINITION  mg49g01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone IMAGE:427152 5', mRNA sequence.
ACCESSION   AA003356
VERSION     AA003356.1  GI:1446796
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1  (bases 1 to 401)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT   On May 8, 1995 this sequence version replaced gi:799469.
          Contact: Marra M/Mouse EST Project
          WashU-HHMI Mouse EST Project
          Washington University School of MedicineP
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          MGI:261704
          Seq primer: ETPrimer
          High quality sequence stop: 345.
FEATURES             Location/Qualifiers
     source          1. .401
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:427152"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /sex="unknown"
                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
                     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                     14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                     State Univ., from 2 ]; double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. Library went through one round of
                     normalization, and was constructed by Bento Soares and
                     M.Fatima Bonaldo.  "
BASE COUNT       92 a     96 c    128 g     85 t
ORIGIN
```

```
  Query Match             14.4%;  Score 214;  DB 27;  Length 401;
  Best Local Similarity   77.5%;  Pred. No. 5.8e-46;
  Matches  259;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy     38 caacaataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaa 97
          ||  |||||| || |||| | |||   |||||  | || || ||||    |||   ||
Db     68 CAGGAATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACG 127

Qy     98 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatca 157
            | | ||| ||    |  | || |||  | |  || ||||||||||||| ||| ||| |
Db    128 GTGCTCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACC 187

Qy    158 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 217
          ||||| || || ||||| ||||||| |||||| |||||||||||||| | |||||| |||
Db    188 GGAGATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAG 247

Qy    218 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 277
          || || || ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    248 TGCGGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAG 307

Qy    278 tgtgtggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 337
          |||||| | ||| ||| |||| |||||||||| |||||||| |||||||| || |||||
```

```
Db    308 TGTGTGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCA 367

Qy    338 tgtctggactgcgcagtggtgaaccgctttcaga 371
          |||  |||||| ||  ||||||||||||| |||||
Db    368 TGTGCGGACTGTGCGCTGGTGAACCGCTGTCAGA 401


RESULT   4
AA036247
LOCUS       AA036247      358 bp    mRNA            EST       26-AUG-1996
DEFINITION  mi74a03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
            IMAGE:472300 5', mRNA sequence.
ACCESSION   AA036247
VERSION     AA036247.1  GI:1509376
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Apr 14, 1993 this sequence version replaced gi:716824.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:283044
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 347.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:472300"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
BASE COUNT       81 a     98 c    110 g     69 t
ORIGIN


  Query Match             12.4%;  Score 185;  DB 27;  Length 358;
  Best Local Similarity   77.5%;  Pred. No. 2.5e-38;
  Matches  224;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy     42 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 101
          |||||| || |||| | |||   |||||  | || || ||||    |||   ||    |
Db     69 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 128

Qy    102 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatcaggag 161
          | ||| ||    |  | || |||  | |  || ||||||||||||| ||| ||| | ||||

Db    129 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 188

Qy    162 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 221
          | || || ||||| ||||||| |||||| |||||||||||||| | |||||| ||||| |
Db    189 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 248

Qy    222 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 281
          | || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    249 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 308

Qy    282 tggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatg 330
          || | ||| ||| |||| |||||||||| |||||||| |||||||| ||
Db    309 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTG 357


RESULT   5
AQ563354
LOCUS       AQ563354      643 bp    DNA             GSS       29-MAY-1999
DEFINITION  HS_5335_B2_B03_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=911 Col=6 Row=D, genomic survey sequence.
ACCESSION   AQ563354
VERSION     AQ563354.1  GI:4922825
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 911  row: D  column: 6
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=911 Col=6 Row=D"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      151 a    154 c    158 g    167 t     13 others
ORIGIN


  Query Match             10.3%;  Score 153.4;  DB 104;  Length 643;
  Best Local Similarity   85.4%;  Pred. No. 6.3e-30;
  Matches  169;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy    509 tgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacg 568
          ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    315 TGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTNCACGGCCTCCAGCCCACGGGACACG 374

Qy    569 gcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcctc 628
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          ||||||     |  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 GCGCTGTGCTGCCGTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTC 434

Qy    629 tgtgtcatctattgtaagagacagtttatggaaaagaaacccagctggtctctgcggtca 688
          ||||||||||||||||||||||||| ||||||  ||||||||||||||        |  |
Db    435 TGTGTCATCTATTGTAAGAGACAGTNTATGGAGAAGAAACCCAGCTGTAAGTGTTGAGCT 494

Qy    689 caggacattcagtacaac 706
          ||  ||||    ||  ||
Db    495 CATTACATNTCTTATCAC 512


RESULT   6
AV111112
LOCUS       AV111112      275 bp    mRNA            EST       29-JUN-1999
DEFINITION  AV111112 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA
            clone 2600016N17, mRNA sequence.
ACCESSION   AV111112
VERSION     AV111112.1  GI:5265192
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 275)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
            Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
            Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
            Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
            Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y.,
            Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
            Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     On Jun 5, 1998 this sequence version replaced gi:3187126.
            Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .275
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="2600016N17"
                     /clone_lib="Mus musculus C57BL/6J 10-day embryo"
                     /sex="mixed"
                     /dev_stage="10-day embryo"
BASE COUNT       77 a     86 c     55 g     57 t
ORIGIN


  Query Match             8.4%;  Score 124.4;  DB 59;  Length 275;
  Best Local Similarity   71.3%;  Pred. No. 2.3e-22;
  Matches  164;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy    309 aggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttc 368
          | ||  | || |||||||| |  ||||| |     ||    ||  ||  ||||| || ||
Db     43 AAGAAAGTGGTTTCCAGAAGTAAAAGCCATTCGCCGAACCTGCCCTGTAGAACCCCTATC 102

Qy    369 agaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccaggatttt 428
          || | |  |||| |||  ||||| ||||||  |||||||||||||| ||||| ||||||
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```
Db    103 TGAGGACCCATTGCTCACACACCACTGATGCACTCTGCGGGGACTGCCTGCCAAGATTTT 162

Qy    429 ataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctc 488
          |   |||||| ||||| || || ||||||||||||||||||||||| || |||||||| |
Db    163 ACCAGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGTGCCCTGCGGAGACCCAC 222

Qy    489 ctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatc 538
          ||||||| |||||||| ||| |||   |    | |||      | ||| |
Db    223 CTCCTCCCTACGAACCACACAGTGAGTGATGTGCCAAGTGGCAGCAGACC 272


RESULT   7
AQ544065
LOCUS       AQ544065      646 bp    DNA             GSS       19-MAY-1999
DEFINITION  RPCI-11-315F10.TV RPCI-11 Homo sapiens genomic clone
            RPCI-11-315F10, genomic survey sequence.
ACCESSION   AQ544065
VERSION     AQ544065.1  GI:4869459
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     On Mar 23, 1999 this sequence version replaced gi:3324949.
            Other_GSSs: RPCI-11-315F10.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .646
                     /organism="Homo sapiens"
                     /db_xref="GDB:7620705"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-315F10"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT       175 a    135 c    145 g    191 t
ORIGIN


  Query Match             8.2%;  Score 122.6;  DB 104;  Length 646;
  Best Local Similarity   93.4%;  Pred. No. 8.4e-22;
  Matches  128;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    675 ggtctctgcggtcacaggacattcagtacaacgagactgagctgtcgtgttttgacagac 734
          |||||||||| |||||||||||||||||||||||||  ||||||||||||||||||||||
Db    263 GGTCTCTGCGGTCACAGGACATTCAGTACAACGGCTCTGAGCTGTCGTGTTTTGACAGAC 322

Qy    735 ctcagctccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcaga 794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 CTCAGCTCCACGAATATGCCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTGCAGA 382
```

```
Qy    795 cctgcgggccggtgcgc 811
          |||||||   | |  ||
Db    383 CCTGCGGTAAGTTCAGC 399


RESULT   8
AA495217
LOCUS       AA495217      404 bp    mRNA            EST       27-JUN-1997
DEFINITION  fa04d10.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 10E17 5', mRNA
            sequence.
ACCESSION   AA495217
VERSION     AA495217.1  GI:2225645
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
            Cyprinoidea; Cyprinidae; Rasborinae; Danio.
REFERENCE   1  (bases 1 to 404)
  AUTHORS   Clark,M., Lehrach,H., Appel,B., Eisen,J., Johnson,S., Marra,M.,
            Eddy,S., Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G.,
            Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Martin,J., Moore,B.,
            Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y.,
            Wylie,T., Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project
  JOURNAL   Unpublished (1997)
COMMENT     On May 9, 1995 this sequence version replaced gi:802250.
            Contact: Steve Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Steve Johnson lab internal ID - P1_332 NOTE - For this library, the
            CLONE id field represents a position identifier on the original
            cDNA library preparation plate. cDNA Library Preparation: Matthew
            Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by:
            Washington University Genome Sequencing Center Clone distribution:
            Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
            Genetik, Berlin Tel +49 30 84 13 1235
            Seq primer: T7 ET from Amersham
            High quality sequence stop: 320.
FEATURES             Location/Qualifiers
     source          1. .404
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="10E17"
                     /clone_lib="Zebrafish ICRFzfls"
                     /sex="mixed"
                     /tissue_type="pooled 26-somite embryos"
                     /lab_host="XL1-blue MRF"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
                     strand cDNA was primed with a Not I - oligo(dT)15 primer
                     [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3'], on
                     mRNA from pooled 26 somite zebrafish embryos;
                     double-stranded cDNA was ligated to Sal I adaptors (BRL),
                     digested with Not I and cloned into the Not I and Sal I
                     sites of the pSPORT1 vector (BRL). Library was constructed
                     by Matthew Clark (Lehrach lab; ICRF, London and  Max
                     Planck Institut fuer Molekulare Genetik, Berlin) and was
                     not biochemically normalised.  70,000 clones from this
                     library were arrayed on high density filters and
                     subsequently screened by oligonucleotide hybridization
                     fingerprinting to identify unique or minimally redundant
                     clones for more intensive analysis."
BASE COUNT       80 a     98 c    125 g    101 t
ORIGIN


  Query Match             7.8%;  Score 116;  DB 34;  Length 404;
  Best Local Similarity   67.0%;  Pred. No. 4.2e-20;
  Matches  197;  Conservative    0;  Mismatches   90;  Indels    7;  Gaps    2;
```

```
Qy    560 cgggacacggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctg 619
          || |||| ||| |||||||| || |||||||| |||||||||| ||||| ||||| ||
Db      1 CGAGACATGGCTCTGGCTGCTGTGATCTGCAGTGCTCTGGCCACTGTCCTCCTGGCGCTC 60

Qy    620 ctcatcctctgtgtcatctattgtaagagacagtttatggaaaagaaacccagctggtct 679
          ||||||||||||| ||||| |||||||||||| |  |||| ||||||||       ||
Db     61 TTCATCCTCTGTGTGATCTACTGTAAGAGACAGCTGCTGGAGAAGAAACC---AGTATCC 117

Qy    680 ctgcggtcacaggacattcagtacaacgagactgagctgtcgtgttttgacagacctcag 739
          || || | || ||    | || |   |  | ||| |||| ||||| ||| |      |
Db    118 ATGAGGGCTCATGAGGGCCCGTTCCTGGGCTCGGAGTTGTCTTGTTTGGACCGGAGAGTG 177

Qy    740 ctccacgaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgc 799
          ||    | |  || ||| ||| ||||||| || |||   | |   ||||  ||||| ||
Db    178 CT----GGAGTTGTCCAGAGACCCTGCTGTCACTGCACTCATAGATCAGGACAGACGTGT 233

Qy    800 gggccggtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaac 853
          ||    || |   || |  | ||  |||| |||||||| | ||| || |  |||
Db    234 GGTGGCGTTCAGCTGGTGTCGTCTGTGTGTTGTGAGGATGTCTGGAGTCAAAAC 287


RESULT   9
AQ514075/c
LOCUS       AQ514075      450 bp    DNA             GSS       05-MAY-1999
DEFINITION  HS_5184_A1_G01_SP6E RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=760 Col=1 Row=M, genomic survey sequence.
ACCESSION   AQ514075
VERSION     AQ514075.1  GI:4746366
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 760  row: M  column: 1
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 450.
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=760 Col=1 Row=M"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
BASE COUNT      156 a     93 c     62 g    137 t      2 others
ORIGIN


  Query Match             7.5%;  Score 112.2;  DB 104;  Length 450;
  Best Local Similarity   93.6%;  Pred. No. 4.3e-19;
  Matches  117;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;
```

```
Qy     128 tatttgtcatgtaaagtgacttgtgaatcaggagactgtagacagcaagaattcagggat 187
           |||  ||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db     327 TATCAGTCATGTAAAGTGACTTGTGATACAGGAGACTGTAGACAGCAAGAATTCAGGGAT 268

Qy     188 cggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaa 247
           |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||| |
Db     267 CGGTCTGGAAAATGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGTA 208

Qy     248 tgtgg 252
           | | |
Db     207 TATTG 203
```

RESULT 10
AI551729
LOCUS AI551729 381 bp mRNA EST 23-MAR-1999
DEFINITION vf11e02.y1 Knowles Solter mouse blastocyst B3 Mus musculus cDNA clone IMAGE:835418 5', mRNA sequence.
ACCESSION AI551729
VERSION AI551729.1 GI:4484092
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 381)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT On Mar 10, 1998 this sequence version replaced gi:2948459.
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:495634
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP.

FEATURES Location/Qualifiers
source 1. .381
/organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:835418"
/clone_lib="Knowles Solter mouse blastocyst B3"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTT-3'. cDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3."

BASE COUNT 105 a 95 c 104 g 77 t
ORIGIN

Query Match 5.3%; Score 78.6; DB 48; Length 381;
Best Local Similarity 55.8%; Pred. No. 3e-10;
Matches 150; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

```
Qy    1042 tcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtc 1101
           ||||||||||||||||||||  |   |||| ||||||||  |||   ||||||  || | ||
Db       1 TCCTGAACTCACTGGAGAAGATACCAATTCCCTCAATCCCGAAAACGAAAGCGCAGCATC 60

Qy    1102 tttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattc 1161
           | ||||||| | | || | || ||| ||| |||    |||| || ||     |||
Db      61 TCTGGATTCCAGTGGCGGCCAGGATCTGGCTGGGACAGCTGCTCTAGAGTCTTCTGGGAA 120

Qy    1162 tgaaaactttacagcagctactgatttatctagatataacaacacactggtagaatcagc 1221
           ||         |  | |   |   |  | | | | |     ||| |    ||    |
Db     121 TGTTTCAGAATCTACTGACTCACCTAGACATGGTGACACTGGTACAGTCTGGGAGCAGAC 180

Qy    1222 atcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgctgtcat 1281
           | |||||||||| | ||  |    ||||||   ||    |||     | |    | |
Db     181 GCTAGCTCAGGATGCTCAAAGGACTCCAAGCCAAGGAGGCTGGGAAGACAGGGAAAACCT 240

Qy    1282 ccacccagccactcagacgtccctccagg 1310
             | | |||||  |  ||  || ||||||
Db     241 GAATCTAGCCATGCCCACAGCCTTCCAGG 269
```

RESULT 11
AL120773
LOCUS AL120773 485 bp mRNA EST 27-SEP-1999
DEFINITION DKFZp762C192_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C192 5', mRNA sequence.
ACCESSION AL120773
VERSION AL120773.1 GI:5926774
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT On Mar 16, 1998 this sequence version replaced gi:2961733.
Contact: Koehrer K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by BMFZ within the cDNA sequencing consortium of the German Genome Project.
No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES Location/Qualifiers
source 1. .485
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp762C192"
/clone_lib="762 (synonym: hmel2)"
/tissue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 150 a 103 c 104 g 128 t
ORIGIN

Query Match 4.2%; Score 61.8; DB 64; Length 485;
Best Local Similarity 90.4%; Pred. No. 8.7e-06;
Matches 66; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy      15 ccaggtggctgggaagaactctccaacaataaatacatttgataagaaagatggctttaa 74
           | | || ||||   ||||||||||||||||||||||||||||||||||||||||||||
Db     413 CTAAGTTGCTGAACGGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGCTTTAA 472

Qy      75 aagtgctactaga 87
```

```
          ||||||||||||||
Db    473 AAGTGCTACTAGA 485


RESULT  12
AQ173919/c
LOCUS       AQ173919      405 bp    DNA             GSS       17-OCT-1998
DEFINITION  HS_3204_A2_C10_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3204 Col=20 Row=E, genomic survey
            sequence.
ACCESSION   AQ173919
VERSION     AQ173919.1  GI:3571286
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3204  row: E  column: 20
            Class: BAC ends
            High quality sequence stop: 405.
FEATURES             Location/Qualifiers
     source          1. .405
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=3204 Col=20 Row=E"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT      109 a     98 c    112 g     85 t      1 others
ORIGIN


  Query Match             4.0%;  Score 59;  DB 99;  Length 405;
  Best Local Similarity   92.5%;  Pred. No. 4.6e-05;
  Matches   62;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    454 tcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgc 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    405 TCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGA 346

Qy    514 cagcaag 520
          | | |
Db    345 GTGAACG 339


RESULT  13
CNS00LPM/c
LOCUS       CNS00LPM     1101 bp    DNA             GSS       03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR32J01 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL068516
VERSION     AL068516.1  GI:4958747
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR32J01"
                     /note="end : TET3"
BASE COUNT      350 a    161 c    165 g    254 t    171 others
ORIGIN


  Query Match             2.9%;  Score 43.4;  DB 79;  Length 1101;
  Best Local Similarity   61.4%;  Pred. No. 0.74;
  Matches   51;  Conservative   10;  Mismatches   22;  Indels    0;  Gaps    0;

Qy   1407 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaattt 1466
           |||||||| |::| ||| || |||| |:|| |||| || |: :| |||||   :| |:|
Db    327 TTTTTTTTAGMWTTTTTTATBATTTATKATTTGTTTTACASCWTTTTTTACTCBATAWTC 268

Qy   1467 caagtatttttttaaaaaacttt 1489
             | ||:|:| :| || || |||
Db    267 TTACTAWTKTAWTGAATAATTTT 245


RESULT  14
AA759377/c
LOCUS       AA759377      443 bp    mRNA            EST       29-DEC-1998
DEFINITION  ah54a10.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309434 3',
            mRNA sequence.
ACCESSION   AA759377
VERSION     AA759377.1  GI:2804852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     On Jan 19, 1998 this sequence version replaced gi:2151262.
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
```

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 587 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 424.

```
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="1309434"
                     /clone_lib="Soares_testis_NHT"
                     /sex="male"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech
                     Laboratories, Inc., and primed with  a Not I - oligo(dT)
                     primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      119 a    107 c    117 g     98 t      2 others
ORIGIN
```

```
  Query Match              2.9%;  Score 42.6;  DB 38;  Length 443;
  Best Local Similarity   65.9%;  Pred. No. 0.99;
  Matches   60;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy    537 tcgcgtccacggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctc 596
          ||| | |||||||| || |   |  | ||| |||||    | | | |||| |  |   | .
Db    416 TCGGGGCCACGGCCGGCATCANNCCCGTCACCGCGCTCTACGGCTTCATCTTCTACCTGC 357

Qy    597 tggccaccgtcctgctggccctgctcatcct 627
          | ||| |||||||||| ||||||| || |
Db    356 TCGCCTCCGTCCTGCTCTCCCTGCTCCTCAT 326
```

```
RESULT  15
CNS009YZ/c
LOCUS       CNS009YZ      806 bp    DNA             GSS       03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR20021 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL054514
VERSION     AL054514.1  GI:4935687
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 806)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .806
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR20021"
                     /note="end : T7"
BASE COUNT      288 a     86 c    116 g    160 t    156 others
ORIGIN
```

```
  Query Match              2.8%;  Score 42.4;  DB 79;  Length 806;
  Best Local Similarity   38.6%;  Pred. No. 1.3;
  Matches   78;  Conservative   34;  Mismatches   90;  Indels    0;  Gaps    0;

Qy   1288 agccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacacagcactg 1347
           ::::|||:::: :||:  | : : : : :|::| ||   | :      : |      |
Db    606 HSMVACTMRKMWVTCMTGCGMCRCRCKCBASYGTCTCYCTCYATACATMTCTAYCATATY 547

Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
           || : :  || ||:  |::|:| | |||: ::| : || :          |   |   |||
Db    546 ACAYTMTMTATATMTMAMYTYTCTMCCCWAYVTCWCATCWMATTTTTTTTTTTTTTTTT 487

Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
           ||||||||   | |||  |  ||| || | | || |    | | ||||    |   |||
Db    486 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 427

Qy   1468 aagtatttttttaaaaaacttt 1489
               | ||||||:  |||: |::
Db    426 TTTTTTTTTTTYTTAAAWTTKK 405
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Search completed: April 23, 2000, 01:49:00
Job time: 1275 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 23, 2000, 21:40:26 ; Search time 28.62 Seconds
(without alignments)
6228.783 Million cell updates/sec

Title: US-09-490-187-1
Perfect score: 1489
Sequence: 1 ggacctgcagcctcccaggt.....gtatttttttaaaaaacttt 1489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 214294 seqs, 59861574 residues

Total number of hits satisfying chosen parameters: 428588

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS9_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	39.6	2.7	4673	1	US-07-638-431-1	Sequence 1, Appli
	2	39.6	2.7	4673	6	PCT-US92-00018-1	Sequence 1, Appli
c	3	36.6	2.5	761	2	US-08-477-877B-83	Sequence 83, Appl
c	4	36.6	2.5	761	2	US-08-472-281A-83	Sequence 83, Appl
c	5	36.6	2.5	761	4	US-08-477-989B-83	Sequence 83, Appl
c	6	36.6	2.5	807	2	US-08-477-877B-90	Sequence 90, Appl
c	7	36.6	2.5	807	2	US-08-472-281A-90	Sequence 90, Appl
c	8	36.6	2.5	807	4	US-08-477-989B-90	Sequence 90, Appl
	9	36.4	2.4	1601	2	US-08-722-001-7	Sequence 7, Appli
	10	36.4	2.4	1987	2	US-08-722-001-26	Sequence 26, Appl
	11	36.4	2.4	1997	2	US-08-722-001-27	Sequence 27, Appl
	12	36.4	2.4	2004	2	US-08-722-001-11	Sequence 11, Appl
	13	36.2	2.4	2485	2	US-08-424-424B-1	Sequence 1, Appli
	14	36.2	2.4	2486	6	PCT-US94-05363A-1	Sequence 1, Appli
c	15	35.4	2.4	1183	4	US-08-705-937-10	Sequence 10, Appl
	16	34.8	2.3	1639	1	US-08-334-698-5	Sequence 5, Appli
	17	34.8	2.3	1639	1	US-08-228-932-5	Sequence 5, Appli
	18	34.8	2.3	1639	2	US-08-468-939-5	Sequence 5, Appli
	19	34.8	2.3	1639	3	US-08-406-855A-5	Sequence 5, Appli
	20	34.8	2.3	1639	4	US-08-722-190-5	Sequence 5, Appli
	21	34.8	2.3	1639	6	PCT-US95-04203-5	Sequence 5, Appli
	22	34.6	2.3	1542	4	US-09-122-230-8	Sequence 8, Appli
	23	34.6	2.3	1909	4	US-09-122-230-6	Sequence 6, Appli
c	24	34.6	2.3	7218	1	US-08-232-463-14	Sequence 14, Appl
c	25	34.2	2.3	19124	4	US-08-487-826B-13	Sequence 13, Appl
c	26	33.8	2.3	568	2	US-08-582-257-20	Sequence 20, Appl
c	27	33.8	2.3	568	3	US-08-582-298-20	Sequence 20, Appl
c	28	33.8	2.3	1493	1	US-08-340-820-24	Sequence 24, Appl
c	29	33.8	2.3	1493	1	US-08-593-535-24	Sequence 24, Appl
c	30	33.8	2.3	1740	2	US-08-362-512A-3	Sequence 3, Appli
c	31	33.8	2.3	2861	1	US-08-299-953-1	Sequence 1, Appli
c	32	33.8	2.3	2861	2	US-08-459-415-1	Sequence 1, Appli
c	33	33.8	2.3	2861	6	PCT-US95-11231-1	Sequence 1, Appli
c	34	33.8	2.3	3881	1	US-08-299-953-2	Sequence 2, Appli
c	35	33.8	2.3	3881	2	US-08-459-415-2	Sequence 2, Appli
c	36	33.8	2.3	3881	6	PCT-US95-11231-2	Sequence 2, Appli
c	37	33.4	2.2	2762	1	US-08-198-446B-12	Sequence 12, Appl
c	38	33.4	2.2	2762	3	US-08-870-693-12	Sequence 12, Appl
c	39	33.2	2.2	1593	1	US-08-307-499-50	Sequence 50, Appl
	40	33.2	2.2	8174	1	US-07-914-281-5	Sequence 5, Appli
	41	33.2	2.2	8174	1	US-08-393-246-5	Sequence 5, Appli
	42	33.2	2.2	8174	2	US-08-525-058A-5	Sequence 5, Appli
	43	33.2	2.2	8174	4	US-08-696-731-5	Sequence 5, Appli
	44	33.2	2.2	8174	6	PCT-US91-00899-3	Sequence 3, Appli
	45	33.2	2.2	14176	1	US-08-307-499-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-07-638-431-1
; Sequence 1, Application US/07638431
; Patent No. 5198535
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Charoenvit, Yupin
; APPLICANT: Hedstrom, Richard
; APPLICANT: Khusmith, Srisin
; APPLICANT: Rogers IV, William O.
; TITLE OF INVENTION: Protective malaria sporozoite surface protein
; TITLE OF INVENTION: immunogen and gene
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: A. David Spevack
; STREET: NMRDC Building 1 T-12 National Naval
; STREET: Medical Center
; CITY: Bethesda
; STATE: MD
; COUNTRY: USA
; ZIP: 20814-5044
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/638,431
; FILING DATE: 19910110
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Spevack, Avrom D.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-6759
; TELEFAX: (301) 295-4033
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4673 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
; STRAIN: 17X(NL)
; DEVELOPMENTAL STAGE: erythrocytic stage
; TISSUE TYPE: Blood
; CELL TYPE: erythrocytic stage

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;    IMMEDIATE SOURCE:
;      LIBRARY:  Py-lambdagt11-2-7 kb genomic expression
;      CLONE:  Py10.1111
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  718..3195
;      OTHER INFORMATION:
US-07-638-431-1


  Query Match              2.7%;  Score 39.6;  DB 1;  Length 4673;
  Best Local Similarity   60.0%;  Pred. No. 0.085;
  Matches   66;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy   1379 ataagatttgggggaacctggatgagttttttttttttgcatctttaataatttcttatat 1438
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Db   4033 ATATTATTTGTGTAAAAATTAAGATGATATATTTTTAGCATATTTGACAAATTGTCAAAT 4092

Qy   1439 gttgtagagtatgttttaaaataaatttcaagtatttttttaaaaaactt 1488
             |  | | ||||||  || |||| | |    |||||||| |   ||
Db   4093 TCGTTGTATTCTGTTTTTGAAAAAATATGAGCATTTTTTTTAATATTATT 4142


RESULT   2
PCT-US92-00018-1
; Sequence 1, Application PC/TUS9200018
;  GENERAL INFORMATION:
;    APPLICANT:  Hoffman, Stephen L.
;    APPLICANT:  Charoenvit, Yupin
;    APPLICANT:  Hedstrom, Richard
;    APPLICANT:  Khusmith, Srisin
;    APPLICANT:  Rogers IV, William O.
;    TITLE OF INVENTION:  Protective malaria sporozoite surface protein
;    TITLE OF INVENTION:  immunogen and gene encoding
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  A. David Spevack
;      STREET:  NMRDC Building 1 T-12 National Naval
;      STREET:  Medical Center
;      CITY:  Bethesda
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20814-5044
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/00018
;      FILING DATE:  19920103
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spevack, Avram D.
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 295-6759
;      TELEFAX:  (301) 295-4033
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4673 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    ORIGINAL SOURCE:
;      ORGANISM:  Plasmodium yoelii
;      STRAIN:  17X(NL)
;      DEVELOPMENTAL STAGE:  erythrocytic stage
;      TISSUE TYPE:  Blood
;      CELL TYPE:  erythrocytic stage
;    IMMEDIATE SOURCE:
;      LIBRARY:  Py-lambdagt11-2-7 kb genomic expression
;      CLONE:  Py10.1111
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  718..3195
;      OTHER INFORMATION:
PCT-US92-00018-1


  Query Match              2.7%;  Score 39.6;  DB 6;  Length 4673;
  Best Local Similarity   60.0%;  Pred. No. 0.085;
  Matches   66;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy   1379 ataagatttgggggaacctggatgagttttttttttttgcatctttaataatttcttatat 1438
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Db   4033 ATATTATTTGTGTAAAAATTAAGATGATATATTTTTAGCATATTTGACAAATTGTCAAAT 4092

Qy   1439 gttgtagagtatgttttaaaataaatttcaagtatttttttaaaaaactt 1488
             |  | | ||||||  || |||| | |    |||||||| |   ||
Db   4093 TCGTTGTATTCTGTTTTTGAAAAAATATGAGCATTTTTTTTAATATTATT 4142


RESULT   3
US-08-477-877B-83/c
; Sequence 83, Application US/08477877B
; Patent No. 5730979
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,877B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-146
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  761 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
;    FEATURE:
;      NAME/KEY:  Nucleotide sequence encoding LO-CD2a VL chain.
US-08-477-877B-83
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  Query Match             2.5%;  Score 36.6;  DB 2;  Length 761;
  Best Local Similarity   54.0%;  Pred. No. 0.21;
  Matches   75;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
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Db    410 AATTATAATAGATCAGAACAAAGTTATGTGCAAAATTTGCAACCAATCTTTGTGAATTAC 351

Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
          ||||| || |   |||  |       |       |||   ||   |||||||| | ||  |
Db    350 TTTTTGTTACTCATTTCCTGTGAGATCCCGGTGTGTTTTGTGATTTTTAAAAAATATACC 291

Qy   1468 aagtatttttttaaaaaac 1486
          || |  ||||| | |||||
Db    290 AAATGCTTTTTCACAAAAC 272


RESULT   4
US-08-472-281A-83/c
; Sequence 83, Application US/08472281A
; Patent No. 5817311
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,281A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  761 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
;    FEATURE:
;      NAME/KEY:  Nucleotide sequence encoding LO-CD2a VL chain.
US-08-472-281A-83


  Query Match             2.5%;  Score 36.6;  DB 2;  Length 761;
  Best Local Similarity   54.0%;  Pred. No. 0.21;
  Matches   75;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
          | ||| | ||||||||||   |||    ||| ||  |       | | | |   | |
Db    410 AATTATAATAGATCAGAACAAAGTTATGTGCAAAATTTGCAACCAATCTTTGTGAATTAC 351

Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
          ||||| || |   |||  |       |       |||   ||   |||||||| | ||  |
Db    350 TTTTTGTTACTCATTTCCTGTGAGATCCCGGTGTGTTTTGTGATTTTTAAAAAATATACC 291

Qy   1468 aagtatttttttaaaaaac 1486
          || |  ||||| | |||||
Db    290 AAATGCTTTTTCACAAAAC 272


RESULT   5
US-08-477-989B-83/c
; Sequence 83, Application US/08477989B
; Patent No. 5951983
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    APPLICANT:  Kaplan, Ruth
;    APPLICANT:  Kieber-Emmons, Thomas
;    APPLICANT:  Postema, Christina E.
;    APPLICANT:  White-Scharf, Mary
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses
;    TITLE OF INVENTION:  Thereof for Inhibiting
;    TITLE OF INVENTION:  T-Cell Activation and
;    TITLE OF INVENTION:  Proliferation
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,989B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  83:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  761 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  oligonucleotide
;    FEATURE:
;      NAME/KEY:  Nucleotide sequence encoding LO-CD2a
;      NAME/KEY:  VL chain.
US-08-477-989B-83
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  Query Match             2.5%;  Score 36.6;  DB 4;  Length 761;
  Best Local Similarity   54.0%;  Pred. No. 0.21;
  Matches   75;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
          | ||| | ||||||||||||   |||    ||| ||  |       | | | |   | |
Db    410 AATTATAATAGATCAGAACAAAGTTATGTGCAAAATTTGCAACCAATCTTTGTGAATTAC 351

Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
          |||||  || |   |||  |      |       |||   ||   |||||||| | ||  |
Db    350 TTTTTGTTACTCATTTCCTGTGAGATCCCGGTGTGTTTTGTGATTTTTAAAAAATATACC 291

Qy   1468 aagtatttttttaaaaaac 1486
          || |  ||||| | |||||
Db    290 AAATGCTTTTTCACAAAAC 272


RESULT   6
US-08-477-877B-90/c
; Sequence 90, Application US/08477877B
; Patent No. 5730979
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activa
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,877B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-146
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  90:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  807 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  polynucleotide
;    FEATURE:
;      NAME/KEY:  Nucleotide sequence encoding humanized LO-CD2a light chain variable re
US-08-477-877B-90


  Query Match             2.5%;  Score 36.6;  DB 2;  Length 807;
  Best Local Similarity   54.0%;  Pred. No. 0.22;
  Matches   75;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
          | ||| | ||||||||||||   |||    ||| ||  |       | | | |   | |
Db    417 AATTATAATAGATCAGAACAAAGTTATGTGCAAAATTTGCAACCAATCTTTGTGAATTAC 358

Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
          |||||  || |   |||  |      |       |||   ||   |||||||| | ||  |
Db    357 TTTTTGTTACTCATTTCCTGTGAGATCCCGGTGTGTTTTGTGATTTTTAAAAAATATACC 298

Qy   1468 aagtatttttttaaaaaac 1486
          || |  ||||| | |||||
Db    297 AAATGCTTTTTCACAAAAC 279


RESULT   7
US-08-472-281A-90/c
; Sequence 90, Application US/08472281A
; Patent No. 5817311
;  GENERAL INFORMATION:
;    APPLICANT:  Bazin, Herv
;    APPLICANT:  Latinne, Dominique
;    TITLE OF INVENTION:  LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Act
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi, Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,281A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/407,009
;      FILING DATE:  29-MAR-1995
;      APPLICATION NUMBER:  08/119,032
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  08/027,008
;      FILING DATE:  05-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  61750-142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  90:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  807 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  polynucleotide
;    FEATURE:
;      NAME/KEY:  Nucleotide sequence encoding humanized LO-CD2a light chain variable
US-08-472-281A-90


  Query Match             2.5%;  Score 36.6;  DB 2;  Length 807;
  Best Local Similarity   54.0%;  Pred. No. 0.22;
  Matches   75;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
          | ||| | ||||||||||||   |||    ||| ||  |       | | | |   | |
Db    417 AATTATAATAGATCAGAACAAAGTTATGTGCAAAATTTGCAACCAATCTTTGTGAATTAC 358
```

```
Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
          ||||| || |   |||  |      |       |||   ||   |||||||| | ||  |
Db    357 TTTTTGTTACTCATTTCCTGTGAGATCCCGGTGTGTTTTGTGATTTTTAAAAAATATACC 298

Qy   1468 aagtatttttttaaaaaac 1486
          || |  ||||| | |||||
Db    297 AAATGCTTTTTCACAAAAC 279
```

RESULT 8
US-08-477-989B-90/c
; Sequence 90, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polynucleotide
; FEATURE:
; NAME/KEY: Nucleotide sequence encoding
; NAME/KEY: humanized LO-CD2a light chain variable region.
US-08-477-989B-90

Query Match 2.5%; Score 36.6; DB 4; Length 807;
Best Local Similarity 54.0%; Pred. No. 0.22;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Qy   1348 acttacagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttt 1407
          | ||| | |||||||||||   |||    ||| ||  |       | | | |   | |
Db    417 AATTATAATAGATCAGAACAAAGTTATGTGCAAAATTTGCAACCAATCTTTGTGAATTAC 358

Qy   1408 ttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttc 1467
          |||||| || |   |||  |      |       |||   ||   |||||||| | ||  |
Db    357 TTTTTGTTACTCATTTCCTGTGAGATCCCGGTGTGTTTTGTGATTTTTAAAAAATATACC 298

Qy   1468 aagtatttttttaaaaaac 1486
          || |  ||||| | |||||
Db    297 AAATGCTTTTTCACAAAAC 279
```

RESULT 9
US-08-722-001-7
; Sequence 7, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-7

Query Match 2.4%; Score 36.4; DB 2; Length 1601;
Best Local Similarity 52.7%; Pred. No. 0.39;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy    538 cgcgtccacggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctct 597
          || |  |  | ||  | |||      ||  || || ||    |||  ||| |   |||||
Db   1107 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCCGGGCTACGTGCTCTTCTCGGCTCT 1166
```

```
Qy    598 ggccaccgtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttat 657
          || | || ||   ||| | |||  |||| ||   |||| || ||        |  |  |
Db   1167 GGGCTCCTTCTACCTGCCTCTGGCCATCATCCTGGTCATGTACTGCCGCGTCTACGTGGT 1226

Qy    658 ggaaaagaaacccagctggtctctgcggtc 687
          ||  ||||     ||| ||   ||   |||
Db   1227 GGCCAAGAGGGAGAGCCGGGGCCTCAAGTC 1256


RESULT 10
US-08-722-001-26
; Sequence 26, Application US/08722001
; Patent No. 5760054
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Wayne J.
;    APPLICANT:  Huff, Joel R.
;    APPLICANT:  Nerenberg, Jennie B.
;    APPLICANT:  Lee, Hee-Yoon
;    APPLICANT:  Bell, Ian M.
;    TITLE OF INVENTION:  ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/722,001
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,276
;      FILING DATE:  14-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19169Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3462
;      TELEFAX:  (908)594-4720
;      TELEX:  138825
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-722-001-26


  Query Match             2.4%;  Score 36.4;  DB 2;  Length 1987;
  Best Local Similarity   52.7%;  Pred. No. 0.45;
  Matches   79;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy    538 cgcgtccacggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctct 597
          || |  |  | ||  | |||      ||  || || ||    |||  ||| |   |||||
Db   1112 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCCGGGCTACGTGCTCTTCTCGGCTCT 1171

Qy    598 ggccaccgtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttat 657
          || | || ||   ||| | |||  |||| ||   ||||| || ||        |  |  |
Db   1172 GGGCTCCTTCTACCTGCCTCTGGCCATCATCCTGGTCATGTACTGCCGCGTCTACGTGGT 1231

Qy    658 ggaaaagaaacccagctggtctctgcggtc 687
```

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          ||  ||||     ||| ||   ||   |||
Db   1232 GGCCAAGAGGGAGAGCCGGGGCCTCAAGTC 1261


RESULT 11
US-08-722-001-27
; Sequence 27, Application US/08722001
; Patent No. 5760054
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Wayne J.
;    APPLICANT:  Huff, Joel R.
;    APPLICANT:  Nerenberg, Jennie B.
;    APPLICANT:  Lee, Hee-Yoon
;    APPLICANT:  Bell, Ian M.
;    TITLE OF INVENTION:  ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/722,001
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,276
;      FILING DATE:  14-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19169Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3462
;      TELEFAX:  (908)594-4720
;      TELEX:  138825
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1997 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-722-001-27


  Query Match             2.4%;  Score 36.4;  DB 2;  Length 1997;
  Best Local Similarity   52.7%;  Pred. No. 0.45;
  Matches   79;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy    538 cgcgtccacggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctct 597
          || |  |  | ||  | |||      ||  || || ||    |||  ||| |   |||||
Db   1106 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCCGGGCTACGTGCTCTTCTCGGCTCT 1165

Qy    598 ggccaccgtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttat 657
          || | || ||   ||| | |||  |||| ||   ||||| || ||        |  |  |
Db   1166 GGGCTCCTTCTACCTGCCTCTGGCCATCATCCTGGTCATGTACTGCCGCGTCTACGTGGT 1225

Qy    658 ggaaaagaaacccagctggtctctgcggtc 687
          ||  ||||     ||| ||   ||   |||
Db   1226 GGCCAAGAGGGAGAGCCGGGGCCTCAAGTC 1255


RESULT 12
```

```
US-08-722-001-11
; Sequence 11, Application US/08722001
; Patent No. 5760054
;  GENERAL INFORMATION:
;    APPLICANT:  Thompson, Wayne J.
;    APPLICANT:  Huff, Joel R.
;    APPLICANT:  Nerenberg, Jennie B.
;    APPLICANT:  Lee, Hee-Yoon
;    APPLICANT:  Bell, Ian M.
;    TITLE OF INVENTION:  ALPHA1C ADRENERGIC RECEPTOR ANTAGONISTS
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merck & Co., Inc.
;      STREET:  126 Lincoln Avenue
;      CITY:  Rahway
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07065
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/722,001
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,276
;      FILING DATE:  14-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Appollina, Mary A.
;      REGISTRATION NUMBER:  34,087
;      REFERENCE/DOCKET NUMBER:  19169Y
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)594-3462
;      TELEFAX:  (908)594-4720
;      TELEX:  138825
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2004 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-722-001-11


  Query Match             2.4%;  Score 36.4;  DB 2;  Length 2004;
  Best Local Similarity   52.7%;  Pred. No. 0.45;
  Matches   79;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy     538 cgcgtccacggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctct 597
           || |  |  | ||  | |||      ||  || || ||    |||  ||| |   |||||
Db    1107 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCCGGGCTACGTGCTCTTCTCGGCTCT 1166

Qy     598 ggccaccgtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttat 657
           || | || ||   ||| | |||  |||| ||   ||||| || ||        |  |  |
Db    1167 GGGCTCCTTCTACCTGCCTCTGGCCATCATCCTGGTCATGTACTGCCGCGTCTACGTGGT 1226

Qy     658 ggaaaagaaacccagctggtctctgcggtc 687
           ||  ||||     ||| ||   ||   |||
Db    1227 GGCCAAGAGGGAGAGCCGGGGCCTCAAGTC 1256


RESULT  13
US-08-424-424B-1
; Sequence 1, Application US/08424424B
; Patent No. 5759854
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Neurotransmitter Transporter
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,424B
;      FILING DATE:  APRIL 21, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/05363
;      FILING DATE:  MAY 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2485 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
US-08-424-424B-1


  Query Match             2.4%;  Score 36.2;  DB 2;  Length 2485;
  Best Local Similarity   56.2%;  Pred. No. 0.59;
  Matches   68;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy     517 caaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggc 576
           ||   ||| ||   ||  | || || || |||||| |||| |  ||  || || |  |||
Db    2023 CAGCATCATCCAGCTGGGGGTCACGCCCCCGGCCTACAGCGCCTGGATCAAGGAGGAGGC 2082

Qy     577 tgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcat 636
           |||||    || |    | |  ||| |    |   |||| || || |||  |    || |
Db    2083 TGCCGAGCGCTACCTGTATTTCCCCAACTGGCCCATGGCACTCCTGATCACCCTCATCGT 2142

Qy     637 c 637
           |
Db    2143 C 2143


RESULT  14
PCT-US94-05363A-1
; Sequence 1, Application PC/TUS9405363A
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Neurotransmitter Transporter
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
```

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;       COMPUTER:  IBM PS/2
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/05363A
;       FILING DATE:  SUBMITTED HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-118
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2486 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
PCT-US94-05363A-1


  Query Match             2.4%;  Score 36.2;  DB 6;  Length 2486;
  Best Local Similarity   56.2%;  Pred. No. 0.59;
  Matches   68;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy    517 caaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggc 576
          ||   ||| ||   ||  | || || || |||||| |||| |  ||  || || |  |||
Db   2024 CAGCATCATCCAGCTGGGGGTCACGCCCCCGGCCTACAGCGCCTGGATCAAGGAGGAGGC 2083

Qy    577 tgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcat 636
          |||||    || |     | |  ||| |   |   |||| || || |||  |    || |
Db   2084 TGCCGAGCGCTACCTGTATTTCCCCAACTGGCCCATGGCACTCCTGATCACCCTCATCGT 2143

Qy    637 c 637
          |
Db   2144 C 2144


RESULT  15
US-08-705-937-10/c
; Sequence 10, Application US/08705937
; Patent No. 5981841
;  GENERAL INFORMATION:
;     APPLICANT:  Santino, Colleen G.
;     APPLICANT:  Conner, Timothy W.
;     TITLE OF INVENTION:  EARLY SEED 5' REGULATORY SEQUENCE
;     NUMBER OF SEQUENCES:  12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Carmen Rodriguez, Paralegal, Arnold, White & Durkee
;       STREET:  P.O. Box 4433
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  USA
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/705,937
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Nicolas G. Barzoukas.
;       REGISTRATION NUMBER:  38,823
;       REFERENCE/DOCKET NUMBER:  MOBT:018 (38-2(10694)A
;       NAME:  Janelle D. Waack.
;       REGISTRATION NUMBER:  36,300
;       REFERENCE/DOCKET NUMBER:  MOBT:018 (38-2(10694)A
;       NAME:  Barbara S. Kitchell
;       REGISTRATION NUMBER:  33,928
;       REFERENCE/DOCKET NUMBER:  MOBT:018 (38-2(10694)A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (713) 787-1400
;       TELEFAX:  (713) 789-2679
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1183 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-705-937-10


  Query Match             2.4%;  Score 35.4;  DB 4;  Length 1183;
  Best Local Similarity   52.6%;  Pred. No. 0.64;
  Matches   72;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy   1352 acagtagatcagaactctgttcccagcataagatttgggggaacctggatgagttttttt 1411
          | || | ||   ||      |     | |||   |||       ||| | | | |||||||
Db    426 AAAGAATATATTAANNANATGTTAAAAATATATTTTTAACCCTCCTCGTTCAATTTTTTT 367

Qy   1412 ttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaatttcaagt 1471
          || || || .| || | | |  ||| | |  |  |||||||  | ||||||  ||    |
Db    366 TTATGGATGCTAAANAGTGTAATATTTATGTTTCAGTATGTCCTTAAATAATATTTCTTT 307

Qy   1472 atttttttaaaaaactt 1488
          | | |  | ||   ||
Db    306 TTGTATGGATAACTATT 290


Search completed: April 23, 2000, 02:01:41
Job time: 1275 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 23, 2000, 01:41:21 ; Search time 42.52 Seconds
(without alignments)
8761.430 Million cell updates/sec

Title: US-09-490-187-1
Perfect score: 1489
Sequence: 1 ggacctgcagcctcccaggt.....gtatttttttaaaaaacttt 1489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1489	100.0	1489	1	X23415	Human hAPO4-alpha
	2	1421.4	95.5	1496	1	V33362	Nucleotide sequenc
	3	1300.8	87.4	2185	1	X24978	Human TRAIN-R cDNA
	4	1268.4	85.2	1704	1	V33361	Nucleotide sequenc
	5	733	49.2	1678	1	X23413	Mouse mAPO4-alpha
	6	457.6	30.7	886	1	X23414	Mouse mAPO4-alpha
	7	457.6	30.7	942	1	X24977	Mouse TRAIN-R (lon
	8	360	24.2	371	1	V11422	Human secreted pro
	9	325	21.8	591	1	X23417	Mouse mAPO4-gamma
	10	325	21.8	599	1	X24976	Mouse TRAIN-R (sho
	11	120.2	8.1	1133	1	X23416	Rat rAPO4-alpha DN
	12	90.4	6.1	791	1	X24979	Clone GJ156 encodi
	13	87.4	5.9	181	1	V11423	Human secreted pro
	14	87.4	5.9	201	1	V86655	EST clone AX92. Ne
	15	80.4	5.4	396	1	X23418	Mouse mAPO4-beta D
	16	39.6	2.7	4673	1	Q27189	P. yoelii SSP2 ant
c	17	38.6	2.6	1558	1	T28255	Survival motor neu
c	18	38.6	2.6	1560	1	T18828	Human survival mot
c	19	38.6	2.6	1582	1	T18831	Human survival mot
c	20	38.6	2.6	1582	1	T28259	Survival motor neu
	21	38.4	2.6	326	1	Q05546	Fragment 41-3 of t
	22	38.2	2.6	4315	1	V80619	Kidney injury asso
	23	37.4	2.5	5805	1	X20268	Borrelia burgdorfe
c	24	36.8	2.5	1453	1	N91505	Maize 33c BamHI fr
c	25	36.6	2.5	761	1	V22851	LO-CD2a light chai
c	26	36.6	2.5	761	1	V62663	LO-CD2a antibody V
c	27	36.6	2.5	807	1	V62665	Humanised LO-CD2a
	28	36.4	2.4	1602	1	Q72217	Human adrenergic r
	29	36.4	2.4	1978	1	Q72212	Truncated human al
	30	36.4	2.4	1987	1	T11624	Human truncated al
	31	36.4	2.4	1997	1	T11600	Human alpha-1C adr
	32	36.4	2.4	1998	1	Q72213	Human alpha-1C adr
	33	36.4	2.4	2004	1	T11599	Human alpha-1C adr
	34	36.4	2.4	2005	1	Q72211	Human alpha-1C adr
	35	36.2	2.4	2486	1	T09866	Human neurotransmi
	36	36	2.4	1193	1	V74563	Staphylococcus aur
c	37	36	2.4	2067	1	V99092	DNA methyltransfer
c	38	36	2 4	19440	1	V99129	DNA methyltransfer
c	39	35.6	2.4	761	1	Q71876	LO-CD2a VL coding
c	40	35.4	2.4	1183	1	V29221	Nucleotide sequenc
c	41	35	2.4	403	1	T29006	Parietaria allerge
c	42	35	2.4	845	1	Q03998	Sequence complemen
	43	34.8	2 3	1639	1	Q63182	Alpha 1c adrenergi
	44	34.8	2 3	1639	1	Q62818	Genomic sequence e
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ALIGNMENTS

RESULT 1
X23415
ID X23415 standard; DNA; 1489 BP.
AC X23415;
DT 18-JUN-1999 (first entry)
DE Human hAPO4-alpha DNA.
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; APO4-alpha; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 65. .1336
FT /*tag= a
FT /product= "hAPO4-alpha"
PN WO9911791-A2.
PD 11-MAR-1999.
PF 04-SEP-1998; 98WO-US18393.
PR 05-SEP-1997; 97US-924634.
PA (UNIW) UNIV WASHINGTON.
PI Chaudhary PM;
DR WPI; 99-205191/17.
DR P-PSDB; W93581.
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
PS Example IV; Fig 7C; 156pp; English.
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
SQ Sequence 1489 BP; 361 A; 366 C; 380 G; 382 T;

Query Match 100.0%; Score 1489; DB 1; Length 1489;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggacctgcagcctcccaggtggctgggaagaactctccaacaataaatacatttgataag 60

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Db      1 GGACCTGCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAG 60

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Qy    121 actaggctatttgtcatgtaaagtgacttgtgaatcaggagactgtagacagcaagaatt 180
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Qy    181 cagggatcggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtc 240
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Qy    241 taaggaatgtggcttcggctatggggaggatgcacagtgtgtggcgtgccggctgcacag 300
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Qy    361 ccgctttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgcc 420
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Qy    421 aggattttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtgg 480
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Qy    481 agaccctcctcctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgc 540
Db    481 AGACCCTCCTCCTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGC 540

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Db    541 GTCCACGGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGC 600

Qy    601 caccgtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttatgga 660
Db    601 CACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCATCTATTGTAAGAGACAGTTTATGGA 660

Qy    661 aaagaaacccagctggtctctgcggtcacaggacattcagtacaacgagactgagctgtc 720
Db    661 AAAGAAACCCAGCTGGTCTCTGCGGTCACAGGACATTCAGTACAACGAGACTGAGCTGTC 720

Qy    721 gtgttttgacagacctcagctccacgaatatgcccacagagcctgctgccagtgccgccg 780
Db    721 GTGTTTTGACAGACCTCAGCTCCACGAATATGCCCACAGAGCCTGCTGCCAGTGCCGCCG 780

Qy    781 tgactcagtgcagacctgcgggccggtgcgcttgctcccatccatgtgctgtgaggaggc 840
Db    781 TGACTCAGTGCAGACCTGCGGGCCGGTGCGCTTGCTCCCATCCATGTGCTGTGAGGAGGC 840

Qy    841 ctgcagccccaacccggcgactcttggttgtggggtgcattctgcagccagtcttcaggc 900
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Qy    901 aagaaacgcaggcccagccggggagatggtgccgactttcttcggatccctcacgcagtc 960
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Qy   1441 tgtagagtatgttttaaaataaatttcaagtatttttttaaaaaacttt 1489
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RESULT 2
V33362
ID V33362 standard; cDNA to mRNA; 1496 BP.
AC V33362;
DT 02-DEC-1998 (first entry)
DE Nucleotide sequence of human beta-OAF065.
KW Human; beta-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
OS Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	45. .1316
FT		/*tag= a
FT		/product= "human beta-OAF065 protein"
FT	sig_peptide	45. .119
FT		/*tag= b
FT	mat_peptide	120. .1313
FT		/*tag= c
FT		/transl_except= (pos:711. .713, aa= Pro)
FT		/transl_except= (pos:714. .716, aa= Arg)

PN WO9838304-A1.
PD 03-SEP-1998.
PF 26-FEB-1998; J00799.
PR 27-FEB-1997; JP-043143.
PA (ONOY) ONO PHARM CO LTD.
PI Fukushima D, Konishi M, Tada H;
DR WPI; 98-481205/41.
DR P-PSDB; W70387.
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
PS Disclosure; Pages 40-41; 54pp; Japanese.
CC This is the nucleotide sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T;

Query Match 95.5%; Score 1421.4; DB 1; Length 1496;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1443; Conservative 0; Mismatches 16; Indels 2; Gaps 1;

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Qy      87 aacaagagaaaacgtttttcactcttttagtattactaggctatttgtcatgtaaagtga 146
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Db      67 AACAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTTGTCATGTAAAGTGA 126

Qy     147 cttgtgaatcaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 206
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Qy     207 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 266
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Qy     267 aggatgcacagtgtgtggcgtgccggctgcacaggttcaaggaggactggggcttccaga 326
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Qy     327 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 386
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Qy     387 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 446
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Qy     447 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgc 506
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Qy     507 actgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggaca 566
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Qy     747 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 806
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Qy     807 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     867 gttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggaga 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     927 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 986
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Qy     987 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1046
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Qy    1047 aactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttgg 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1087 ATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTCTCATTCTGAAA 1146

Qy    1167 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1226
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Qy    1287 cagccactcagacgtccctccaggtaaggcagcgactgggttccctgtgaacacagcact 1346
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           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    1385 TTTTTTTTTGCATCTTTAATAATTTCTTGTATGTTGTAGAGTATGTTTTAAAATAAATTT 1444

Qy    1467 caagtatttttttaaaaaact 1487
           |||||||||||||| |||||||
Db    1445 CAAGTATTTTTTTTAAAAACT 1465
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RESULT 3
X24978
ID X24978 standard; cDNA; 2185 BP.
AC X24978;
DT 05-JUL-1999 (first entry)
DE Human TRAIN-R cDNA.
KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 179. .1432
FT /*tag= a
FT sig_peptide 179. .253
FT /*tag= b
FT mat_peptide 254. .1429
FT /*tag= c
PN WO9913078-A1.
PD 18-MAR-1999.
PF 11-SEP-1998; U19030.
PR 06-MAY-1998; US-084422.
PR 12-SEP-1997; US-058631.
PA (BIOJ) BIOGEN INC.
PI Hession C, Tschopp J;
DR WPI; 99-229238/19.
DR P-PSDB; W98146.
PT New cysteine-rich tumor necrosis factor receptor
PS Claim 1; Page 27; 30pp; English.
CC The present sequence encodes a novel human cysteine-rich tumour
CC necrosis factor receptor family member termed TRAIN-R (see W98146).
CC It is a composite of 2 overlapping lambda gt10 clones (GJ159 and
CC GJ158) from a Clontech human adult lung cDNA library. Human
CC TRAIN-R was also cloned from a second sequence subclone of a
CC lambda gt10 cDNA (GJ156, see X24979). Human TRAIN-R is expressed
CC at low levels in every tissue and cell line tested thus far, with
CC higher expression detected in heart, prostate, ovary, testis,
CC peripheral blood lymphocytes, thyroid and adrenal gland.
CC Cell death can be induced by administering an agent capable of
CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
CC of treating, or reducing, the advancement, severity or effects of
CC an immunological disease in a mammal comprises administering a
CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
CC produce a fusion protein which may be targeted to various sites.
CC It can be used in binding assays, and to identify antagonists and
CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
CC severity of an immune response or to treat cancer. TRAIN-R
CC blocking agents can also be used to reduce the severity or effects

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CC   of an immunological disease (all claimed).
SQ   Sequence   2185 BP;    546 A;    551 C;    550 G;    538 T;

  Query Match            87.4%;  Score 1300.8;  DB 1;  Length 2185;
  Best Local Similarity  99.5%;  Pred. No. 0;
  Matches 1305;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 ggacctgcagcctcccaggtggctgggaagaactctccaacaataaatacatttgataag 60
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Db    115 GGACCTGCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAG 174

Qy     61 aaagatggctttaaaagtgctactagaacaagagaaaacgtttttcactctttagtatt 120
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Db    175 AAAGATGGCTTTAAAAGTGCTACTAGAACAAGAGAAAACGTTTTTCACTCTTTTAGTATT 234

Qy    121 actaggctatttgtcatgtaaagtgacttgtgaatcaggagactgtagacagcaagaatt 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    235 ACTAGGCTATTTGTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATT 294

Qy    181 cagggatcggtctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtc 240
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Db    295 CAGGGATCGGTCTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTC 354

Qy    241 taaggaatgtggcttcggctatggggaggatgcacagtgtgtggcgtgccggctgcacag 300
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Db    355 TAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAG 414

Qy    301 gttcaaggaggactggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaa 360
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Qy    361 ccgctttcagaaggcaaattgttcagccaccagtgatgccatctgcggggactgcttgcc 420
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Qy    421 aggattttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtgg 480
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Qy    481 agaccctcctcctcctcttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgc 540
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Qy    541 gtccacggcctccagcccacgggacacggcgctggctgccgttatctgcagcgctctggc 600
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Db    655 GTCCACGGCCTCCAGCCCACGGGACACGGCGCTGGCTGCCGTTATCTGCAGCGCTCTGGC 714

Qy    601 caccgtcctgctggccctgctcatcctctgtgtcatctattgtaagagacagtttatgga 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    715 CACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCATCTATTGTAAGAGACAGTTTATGGA 774

Qy    661 aaagaaacccagctggtctctgcggtcacaggacattcagtacaacgagactgagctgtc 720
          |||||||||||||||||||||||| |||||||||||||||||   ||||||||||
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Qy    721 gtgttttgacagacctcagctccacgaatatgcccacagagcctgctgccagtgccgccg 780
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Db    835 GTGTTTTGACAGACCTCAGCTCCACGAATATGCCCACAGAGCCTGCTGCCAGTGCCGCCG 894

Qy    781 tgactcagtgcagacctgcgggccggtgcgcttgctcccatccatgtgctgtgaggaggc 840
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Db    895 TGACTCAGTGCAGACCTGCGGGCCGGTGCGCTTGCTCCCATCCATGTGCTGTGAGGAGGC 954

Qy    841 ctgcagccccaacccggcgactcttggttgtggggtgcattctgcagccagtcttcaggc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    955 CTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCCAGTCTTCAGGC 1014

Qy    901 aagaaacgcaggcccagccggggagatggtgccgactttcttcggatccctcacgcagtc 960
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Db   1015 AAGAAACGCAGGCCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTCACGCAGTC 1074

Qy    961 catctgtggcgagttttcagatgcctggcctctgatgcagaatcccatgggtggtgacaa 1020
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Qy    1021 catctctttttgtgactcttatcctgaactcactggagaagacattcattctctcaatcc 1080
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Db    1135 CATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAATCC 1194

Qy    1081 agaacttgaaagctcaacgtctttggattcaaatagcagtcaagatttggttggtggggc 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1195 AGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGC 1254

Qy    1141 tgttccagtccagtctcattctgaaaactttacagcagctactgatttatctagatataa 1200
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Db    1255 TGTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAA 1314

Qy    1201 caacacactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctaga 1260
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Db    1315 CAACACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGA 1374

Qy    1261 tcaggagagtggcgctgtcatccacccagccactcagacgtccctccaggta 1312
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Db    1375 TCAGGAGAGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGAA 1426


RESULT   4
V33361
ID   V33361 standard; cDNA to mRNA; 1704 BP.
AC   V33361;
DT   02-DEC-1998  (first entry)
DE   Nucleotide sequence of human alpha-OAF065.
KW   Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW   cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             45. .1298
FT                   /*tag= a
FT                   /product= "human alpha-OAF065 protein"
FT   sig_peptide     45. .119
FT                   /*tag= b
FT   mat_peptide     120. .1295
FT                   /*tag= c
FT                   /transl_except= (pos:711. .713, aa= Pro)
FT                   /transl_except= (pos:714. .716, aa= Arg)
PN   WO9838304-A1.
PD   03-SEP-1998.
PF   26-FEB-1998; J00799.
PR   27-FEB-1997; JP-043143.
PA   (ONOY ) ONO PHARM CO LTD.
PI   Fukushima D, Konishi M, Tada H;
DR   WPI; 98-481205/41.
DR   P-PSDB; W70386.
PT   Membrane polypeptide expressed by human stroma cells, and antibodies
PT   recognising it - for treatment of inflammatory and other
PT   cytokine-mediated diseases.
PS   Claim 5; Pages 31-32; 54pp; Japanese.
CC   This is the nucleotide sequence of the human alpha-OAF065, used in
CC   the method of the invention.  The process involves the use of peptides
CC   expressed by stroma cells, and its antibodies are used for in the
CC   prevention and treatment of inflammatory and other cytokine-mediated
CC   diseases such as rheumatism, ulcerative colitis.
SQ   Sequence   1704 BP;    429 A;    426 C;    430 G;    419 T;

  Query Match            85.2%;  Score 1268.4;  DB 1;  Length 1704;
  Best Local Similarity  99.1%;  Pred. No. 0;
  Matches 1275;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy     27 gaagaactctccaacaataaatacatttgataagaaagatggctttaaaagtgctactag 86
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Db      7 GTAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGCTTTAAAAGTGCTACTAG 66

Qy     87 aacaagagaaaacgtttttcactctttagtattactaggctatttgtcatgtaaagtga 146
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Db      67 AACAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTTGTCATGTAAAGTGA 126

Qy     147 cttgtgaatcaggagactgtagacagcaagaattcagggatcggtctggaaactgtgttc 206
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Db     127 CTTGTGAAACAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGGAAACTGTGTTC 186

Qy     207 cctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtggcttcggctatgggg 266
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Qy     267 aggatgcacagtgtgtggcgtgccggctgcacaggttcaaggaggactggggcttccaga 326
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Db     247 AGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTCCAGA 306

Qy     327 aatgcaagccctgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcag 386
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Db     307 AATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCAG 366

Qy     387 ccaccagtgatgccatctgcggggactgcttgccaggattttataggaagacgaaacttg 446
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Db     367 CCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTG 426

Qy     447 tcggctttcaagacatggagtgtgtgccttgtggagaccctcctcctcctcttacgaaccgc 506
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Db     427 TCGGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGC 486

Qy     507 actgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcctccagcccacgggaca 566
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Db     487 ACTGTGCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACA 546

Qy     567 cggcgctggctgccgttatctgcagcgctctggccaccgtcctgctggccctgctcatcc 626
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Qy     627 tctgtgtcatctattgtaagagacagtttatggaaaagaaacccagctggtctctgcggt 686
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Db     607 TCTGTGTCATCTATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGT 666

Qy     687 cacaggacattcagtacaacgagactgagctgtcgtgttttgacagacctcagctccacg 746
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Db     667 CACAGGACATTCAGTACAACGGCTCTGAGCTGTCGTGTCTTGACAGACCTCAGCTCCACG 726

Qy     747 aatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccgg 806
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Db     727 AATATGCCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCCG 786

Qy     807 tgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactcttg 866
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Db     787 TGCGCTTGCTCCCATCCATGTGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTG 846

Qy     867 gttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccgggggaga 926
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Qy     927 tggtgccgactttcttcggatccctcacgcagtccatctgtggcgagttttcagatgcct 986
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Db     907 TGGTGCCGACTTTCTTCGGATCCCTCACGCAGTCCATCTGTGGCGAGTTTTCAGATGCCT 966

Qy     987 ggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcctg 1046
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Db     967 GGCCTCTGATGCAGAATCCCATGGGTGGTGACAACATCTCTTTTTGTGACTCTTATCCTG 1026

Qy    1047 aactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttgg 1106
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Db    1027 AACTCACTGGAGAAGACATTCATTCTCTCAATCCAGAACTTGAAAGCTCAACGTCTTTGG 1086

Qy    1107 attcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaaa 1166
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Db    1087 ATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCTGTTCCAGTCCAGTCTCATTCTGAAA 1146

Qy    1167 actttacagcagctactgatttatctagatataacaacacactggtagaatcagcatcaa 1226
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Qy    1227 ctcaggatgcactaactatgagaagccagctagatcaggagagtggcgctgtcatccacc 1286
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Db    1207 CTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGCGCTATCATCCACC 1266

Qy    1287 cagccactcagacgtccctccaggta 1312
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Db    1267 CAGCCACTCAGACGTCCCTCCAGGAA 1292
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RESULT 5
X23413
ID X23413 standard; DNA; 1678 BP.
AC X23413;
DT 18-JUN-1999 (first entry)
DE Mouse mAPO4-alpha (long) DNA.
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; mAPO4-alpha; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 72. .1322
FT /*tag= a
FT /product= "mAPO4-alpha"
PN WO9911791-A2.
PD 11-MAR-1999.
PF 04-SEP-1998; U18393.
PR 05-SEP-1997; US-924634.
PA (UNIW) UNIV WASHINGTON.
PI Chaudhary PM;
DR WPI; 99-205191/17.
DR P-PSDB; W93579.
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
PS Example IV; Fig 7A; 156pp; English.
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents. useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
SQ Sequence 1678 BP; 371 A; 467 C; 466 G; 374 T;

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  Query Match             49.2%;  Score 733;  DB 1;  Length 1678;
  Best Local Similarity   74.2%;  Pred. No. 1.3e-199;
  Matches  941;  Conservative    0;  Mismatches  325;  Indels    3;  Gaps    1;

Qy      42 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 101
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Db      49 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 108

Qy     102 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatcaggag 161
           | ||| ||    |  | || |||  | |  || ||||||||||| ||| ||| | ||||
Db     109 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 168
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Qy    162 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 221
Db    169 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 228

Qy    222 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 281
Db    229 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 288

Qy    282 tggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 341
Db    289 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 348

Qy    342 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 401
Db    349 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 408

Qy    402 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 461
Db    409 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 468

Qy    462 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 521
Db    469 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 528

Qy    522 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 581
Db    529 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 588

Qy    582 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 641
Db    589 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 648

Qy    642 gtaagagacagtttatggaaaagaaacccagctggtctctgcggtcacaggacattcagt 701
Db    649 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCACAGGACATTCAGT 708

Qy    702 acaacgagactgagctgtcgtgttttgacagacctcagctccacgaatatgcccacagag 761
Db    709 ACAATGGCTCTGAGCTGTCATGCTTTGACCAGCCTCGGCTCCGCCACTGTGCCCATAGAG 768

Qy    762 cctgctgccagtgccgccgtgactcagtgcagacctgcgggccggtgcgcttgctcccat 821
Db    769 CATGCTGTCAGTATCACCGGGACTCAGCCCCAATGTATGGGCCTGTTCACCTGATTCCGT 828

Qy    822 ccatgtgctgtgaggaggcctgcagccccaacccggcgactcttggttgtggggtgcatt 881
Db    829 CCTTGTGCTGTGAAGAGGCCCGCAGCTCTGCCCGAGCTGTGCTTGGCTGTGGGCTGCGTT 888

Qy    882 ctgcagccagtcttcaggcaagaaacgcaggcccagccggggagatggtgccgactttct 941
Db    889 CTCCCACTACCCTCCAGGAGAGAAACCCGGCTTCTGTGGGGAACACGATGCCAGCCTTCT 948

Qy    942 tcggatccctcacgcagtccatctgtggcgagttttcagatgcctggcctctgatgcaga 1001
Db    949 TTGGGTCTGTTTCCCGTTCCATCTGCGCGGAGTTTTCTGATGCCTGGCCTCTGATGCAGA 1008

Qy   1002 atcccatgggtggtgacaacatctctttttgtgactcttatcctgaactcactggagaag 1061
Db   1009 ATCCTCTGGGCGGTG---ACAGCTCTCTCTGTGACTCTTATCCTGAACTCACTGGAGAAG 1065

Qy   1062 acattcattctctcaatccagaacttgaaagctcaacgtctttggattcaaatagcagtc 1121
Db   1066 ATACCAATTCCCTCAATCCCGAAAACGAAAGCACAGCATCTCTGGATTCCAGTGGCGGCC 1125

Qy   1122 aagatttggttggtggggctgttccagtccagtctcattctgaaaactttacagcagcta 1181
Db   1126 AGGATCTGGCTGGGACAGCTGCTCTAGAGTCTTCTGGGAATGTTTCAGAATCTACTGACT 1185

Qy   1182 ctgatttatctagatataacaacacactggtagaatcagcatcaactcaggatgcactaa 1241
Db   1186 CACCTAGACATGGTGACACTGGTACAGTCTGGGAGCAGACGCTAGCTCAGGATGCTCAAA 1245

Qy   1242 ctatgagaagccagctagatcaggagagtggcgctgtcatccacccagccactcagacgt 1301
Db   1246 GGACTCCAAGCCAAGGAGGCTGGGAAGACAGGGAAAACCTGAATCTAGCCATGCCCACAG 1305

Qy   1302 ccctccagg 1310
Db   1306 CCTTCCAGG 1314
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RESULT 6
X23414
ID X23414 standard; DNA; 886 BP.
AC X23414;
DT 18-JUN-1999 (first entry)
DE Mouse mAPO4-alpha (short) DNA.
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormalitity; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; mAPO4-alpha; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 72. .716
FT /*tag= a
FT /product= "mAPO4-alpha short"
PN WO9911791-A2.
PD 11-MAR-1999.
PF 04-SEP-1998; U18393.
PR 05-SEP-1997; US-924634.
PA (UNIW) UNIV WASHINGTON.
PI Chaudhary PM;
DR WPI; 99-205191/17.
DR P-PSDB; W93580.
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
PS Example IV; Fig 7B; 156pp; English.
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
SQ Sequence 886 BP; 204 A; 245 C; 247 G; 190 T;

Query Match 30.7%; Score 457.6; DB 1; Length 886;
Best Local Similarity 81.6%; Pred. No. 4.5e-121;
Matches 529; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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Qy     42 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 101
Db     49 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 108

Qy    102 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatcaggag 161
Db    109 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 168
```

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Qy    162 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 221
          | || || ||||| ||||||| |||||| ||||||||||||| | |||||| ||||| |
Db    169 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 228

Qy    222 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 281
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Db    229 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 288

Qy    282 tggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 341
          || | ||| ||| |||| |||||||||| |||||||| |||||||| || ||||| |||
Db    289 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 348

Qy    342 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 401
          ||||||  ||  ||||||||||||||||||| ||| || || |||  ||||||||||||
Db    349 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 408

Qy    402 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 461
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Db    409 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 468

Qy    462 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 521
          |||||||||||| || |||||||| |||||||| |||||||| |||||| ||||||||||
Db    469 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 528

Qy    522 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 581
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Db    529 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 588

Qy    582 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 641
          | |||||||| |||||||||| || ||||| |||||||||||||| ||||||||||| |
Db    589 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 648

Qy    642 gtaagagacagtttatggaaaagaaacccagctggtctctgcggtcac 689
          | ||||| ||||| ||||| ||||||||||||||    || |  || |
Db    649 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCC 696
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RESULT 7
X24977
ID X24977 standard; cDNA; 942 BP.
AC X24977;
DT 05-JUL-1999 (first entry)
DE Mouse TRAIN-R (long form) cDNA.
KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 101. .745
FT /*tag= a
PN WO9913078-A1.
PD 18-MAR-1999.
PF 11-SEP-1998; U19030.
PR 06-MAY-1998; US-084422.
PR 12-SEP-1997; US-058631.
PA (BIOJ) BIOGEN INC.
PI Hession C, Tschopp J;
DR WPI; 99-229238/19.
DR P-PSDB; W98145.
PT New cysteine-rich tumor necrosis factor receptor
PS Claim 1; Page 26-27; 30pp; English.
CC The present sequence encodes a novel murine cysteine-rich tumour
CC necrosis factor receptor family member termed TRAIN-R (long form)
CC (see W98145). Murine TRAIN-R is expressed at high levels in brain
CC and lung, and at lower levels in liver, skeletal muscle and kidney.
CC Cell death can be induced by administering an agent capable of
CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
CC of treating, or reducing, the advancement, severity or effects of
CC an immunological disease in a mammal comprises administering a
CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC e.g. soluble TRAIN-R (see also W98144). TRAIN-R can be fused to an
CC immunoglobulin molecule to produce a fusion protein which may be
CC targeted to various sites. It can be used in binding assays, and
CC to identify antagonists and agonists. Anti-TRAIN receptor
CC antibodies can be used to reduce the severity of an immune response
CC or to treat cancer. TRAIN-R blocking agents can be used to reduce
CC the severity or effects of an immunological disease (all claimed).
SQ Sequence 942 BP; 219 A; 264 C; 258 G; 200 T;

Query Match 30.7%; Score 457.6; DB 1; Length 942;
Best Local Similarity 81.6%; Pred. No. 4.7e-121;
Matches 529; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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Qy     42 aataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgt 101
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Db     78 AATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACGGTGC 137

Qy    102 ttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatcaggag 161
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Db    138 TCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACCGGAG 197

Qy    162 actgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccagtgtg 221
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Db    198 ATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGCG 257

Qy    222 ggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacagtgtg 281
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Db    258 GACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGTG 317

Qy    282 tggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccctgtc 341
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Db    318 TGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCATGTG 377

Qy    342 tggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgatgcca 401
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Db    378 CGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGATGCTG 437

Qy    402 tctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaagaca 461
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Db    438 TCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAAGACA 497

Qy    462 tggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaagg 521
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Db    498 TGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCAGCAAGG 557

Qy    522 tcaacctcgtgaagatcgcgtccacggcctccagcccacgggacacggcgctggctgccg 581
          | ||||| |||||||| | ||||| | |||||||| ||||||||||||||||||||||||
Db    558 TGAACCTTGTGAAGATCTCCTCCACCGTCTCCAGCCCTCGGGACACGGCGCTGGCTGCCG 617

Qy    582 ttatctgcagcgctctggccaccgtcctgctggccctgctcatcctctgtgtcatctatt 641
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Db    618 TCATCTGCAGTGCTCTGGCCACGGTGCTGCTCGCCCTGCTCATCCTGTGTGTCATCTACT 677

Qy    642 gtaagagacagtttatggaaaagaaacccagctggtctctgcggtcac 689
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Db    678 GCAAGAGGCAGTTCATGGAGAAGAAACCCAGCTGTAAGCTCCCATCCC 725
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RESULT 8
V11422
ID V11422 standard; cDNA; 371 BP.
AC V11422;
DT 23-JUL-1998 (first entry)
DE Human secreted protein clone AX92_3 cDNA 5'-end.
KW Secreted protein; prevention; treatment; gene therapy; ds.
OS Homo sapiens.
PN WO9801554-A2.
PD 15-JAN-1998.
PF 07-JUL-1997; U11876.
PR 09-JUL-1996; US-677231.
PA (GEMY) GENETICS INST INC.
PI Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM,
PI Merberg D, Racie LA, Spaulding V, Treacy M;
DR WPI; 98-110230/10.
DR P-PSDB; W58844.

```
PT   Secreted proteins and polynucleotides encoding them - useful to
PT   prevent, treat and ameliorate medical conditions
PS   Claim 15; Page 57; 93pp; English.
CC   V11422-V11424 encode fragments of a novel secreted protein derived from
CC   clone AX92_3 which was isolated from a human adult testes cDNA library.
CC   The protein can be used to prevent, treat or ameliorate a medical
CC   condition, while the polynucleotides can be used for gene therapy.
SQ   Sequence   371 BP;    83 A;    96 C;    107 G;    82 T;


  Query Match             24.2%;  Score 360;  DB 1;  Length 371;
  Best Local Similarity   97.8%;  Pred. No. 2.1e-93;
  Matches  363;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy    192 ctggaaactgtgttccctgcaaccagtgtgggccaggcatggagttgtctaaggaatgtg 251
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Db      1 CTGGAAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTG 60

Qy    252 gcttcggctatggggaggatgcacagtgtgtggcgtgccggctgcacaggttcaaggagg 311
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Db     61 GCTTCGGCTATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGG 120

Qy    312 actggggcttccagaaatgcaagccctgtctggactgcgcagtggtgaaccgctttcaga 371
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Db    121 ACTGGGGCTTCCAAAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGA 180

Qy    372 aggcaaattgttcagccaccagtgatgccatctgcggggactgcttgccaggattttata 431
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    181 AGGCAAATTGTTCAGCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCANGATTTTATA 240

Qy    432 ggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggagaccctcctc 491
          ||||||| |||||||||||||||||| |||||||||||||||||||||| |||||||||
Db    241 GGAAGACNAAACTTGTCGGCTTTCAAAACATGGAGTGTGTGCCTTGTGGAAACCCTCCTC 300

Qy    492 ctccttacgaaccgcactgtgccagcaaggtcaacctcgtgaagatcgcgtccacggcct 551
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Db    301 CTCCTTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTGAAAATCNCGTCCACGGCCT 360

Qy    552 ccagcccacgg 562
          ||||||||||||
Db    361 CCAGCCCACGG 371


RESULT   9
X23417
ID   X23417 standard; DNA; 591 BP.
AC   X23417;
DT   18-JUN-1999  (first entry)
DE   Mouse mAPO4-gamma DNA.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; APO4-gamma; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             95. .547
FT                   /*tag=  a
FT                   /product= "mAPO4-gamma"
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   P-PSDB; W93583.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Disclosure; Fig 7E; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
SQ   Sequence   591 BP;    148 A;    145 C;    175 G;    123 T;


  Query Match             21.8%;  Score 325;  DB 1;  Length 591;
  Best Local Similarity   78.0%;  Pred. No. 2.8e-83;
  Matches  391;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy     38 caacaataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaa 97
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Db     68 CAGGAATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACG 127

Qy     98 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatca 157
            | | ||| ||    |  | || |||  | |  || ||||||||||| ||| ||| |
Db    128 GTGCTCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACC 187

Qy    158 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 217
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Db    188 GGAGATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAG 247

Qy    218 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 277
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Db    248 TGCGGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAG 307

Qy    278 tgtgtggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 337
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Db    308 TGTGTGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCA 367

Qy    338 tgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgat 397
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Db    368 TGTGCGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGAT 427

Qy    398 gccatctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaa 457
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Db    428 GCTGTCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAA 487

Qy    458 gacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagc 517
          ||||||||||||||||| || |||||||| |||||||| |||||||| |||||||   |
Db    488 GACATGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTGAGTGA 547

Qy    518 aaggtcaacctcgtgaagatc 538
             | |||  .  | ||| |
Db    548 TGTGCCAAGTGGCAGCAGACC 568


RESULT  10
X24976
ID   X24976 standard; cDNA; 599 BP.
AC   X24976;
DT   05-JUL-1999  (first entry)
DE   Mouse TRAIN-R (short form) cDNA.
KW   TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic; ss.
OS   Mus musculus.
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FH   Key             Location/Qualifiers
FT   CDS             104. .556
FT                   /*tag= a
PN   WO9913078-A1.
PD   18-MAR-1999.
PF   11-SEP-1998; U19030.
PR   06-MAY-1998; US-084422.
PR   12-SEP-1997; US-058631.
PA   (BIOJ ) BIOGEN INC.
PI   Hession C, Tschopp J;
DR   WPI; 99-229238/19.
DR   P-PSDB; W98144.
PT   New cysteine-rich tumor necrosis factor receptor
PS   Claim 1; Page 26; 30pp; English.
CC   The present sequence encodes a novel murine cysteine-rich tumour
CC   necrosis factor receptor family member termed TRAIN-R (short form)
CC   (see W98144). This putative natural soluble form of murine TRAIN-R
CC   may inhibit signalling by the full-length TRAIN-R (see W98145).
CC   Murine TRAIN-R is expressed at high levels in brain and lung, and
CC   at lower levels in liver, skeletal muscle and kidney. Cell death
CC   can be induced by administering an agent capable of inhibiting the
CC   binding of TRAIN-R to its ligand. A claimed method of treating, or
CC   reducing, the advancement, severity or effects of an immunological
CC   disease in a mammal comprises administering a pharmaceutical
CC   composition which comprises a TRAIN-R blocking agent, e.g. soluble
CC   TRAIN-R. TRAIN-R can be fused to an immunoglobulin molecule to
CC   produce a fusion protein which may be targeted to various sites.
CC   It can be used in binding assays, and to identify antagonists and
CC   agonists. Anti-TRAIN receptor antibodies can be used to reduce the
CC   severity of an immune response or to treat cancer. TRAIN-R
CC   blocking agents can be used to reduce the severity or effects of an
CC   immunological disease (all claimed).
SQ   Sequence   599 BP;    149 A;    147 C;    180 G;    123 T;

  Query Match            21.8%;  Score 325;  DB 1;  Length 599;
  Best Local Similarity  78.0%;  Pred. No. 2.8e-83;
  Matches  391;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy      38 caacaataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaa 97
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Db      77 CAGGAATAAACACGTTTGGTGAGAGCCATGGCACTCAAGGTCCTACCTCTACACAGGACG 136

Qy      98 acgtttttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatca 157
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Db     137 GTGCTCTTCGCTGCCATTCTCTTCCTACTCCACCTGGCATGTAAAGTGAGTTGCGAAACC 196

Qy     158 ggagactgtagacagcaagaattcagggatcggtctggaaactgtgttccctgcaaccag 217
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Db     197 GGAGATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAG 256

Qy     218 tgtgggccaggcatggagttgtctaaggaatgtggcttcggctatggggaggatgcacag 277
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Db     257 TGCGGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAG 316

Qy     278 tgtgtggcgtgccggctgcacaggttcaaggaggactggggcttccagaaatgcaagccc 337
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Db     317 TGTGTGCCCTGCAGGCCGCACCGGTTCAAGGAAGACTGGGGTTTCCAGAAGTGTAAGCCA 376

Qy     338 tgtctggactgcgcagtggtgaaccgctttcagaaggcaaattgttcagccaccagtgat 397
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Db     377 TGTGCGGACTGTGCGCTGGTGAACCGCTTTCAGAGGGCCAACTGCTCACACACCAGTGAT 436

Qy     398 gccatctgcggggactgcttgccaggattttataggaagacgaaacttgtcggctttcaa 457
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Db     437 GCTGTCTGCGGGGACTGCCTGCCAGGATTTTACCGGAAGACCAAACTGGTTGGTTTTCAA 496

Qy     458 gacatggagtgtgtgccttgtggagaccctcctcctccttacgaaccgcactgtgccagc 517
           |||||||||||||||| || |||||||| |||||||| |||||||| |||||||   |
Db     497 GACATGGAGTGTGTGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTGAGTGA 556

Qy     518 aaggtcaacctcgtgaagatc 538
             | |||      | ||| |
```

```
Db     557 TGTGCCAAGTGGCAGCAGACC 577

RESULT  11
X23416
ID   X23416 standard; DNA; 1133 BP.
AC   X23416;
DT   18-JUN-1999  (first entry)
DE   Rat rAPO4-alpha DNA.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; rat; APO4-alpha; ss.
OS   Rattus sp.
FH   Key             Location/Qualifiers
FT   CDS             1. .330
FT                   /*tag= a
FT                   /product= "rAPO4-alpha"
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   P-PSDB; W93582.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Example IV; Fig 7D; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
SQ   Sequence   1133 BP;    278 A;    275 C;    258 G;    296 T;

  Query Match            8.1%;  Score 120.2;  DB 1;  Length 1133;
  Best Local Similarity  62.8%;  Pred. No. 1.3e-24;
  Matches  204;  Conservative    0;  Mismatches  118;  Indels    3;  Gaps    1;

Qy     986 tggcctctgatgcagaatcccatgggtggtgacaacatctctttttgtgactcttatcct 1045
           ||||||||||||||||||||  |||||||||   ||| |||| | ||||||||||||||
Db       1 TGGCCTCTGATGCAGAATCCTCTGGGTGGTG---ACAGCTCTCTCTGTGACTCTTATCCT 57

Qy    1046 gaactcactggagaagacattcattctctcaatccagaacttgaaagctcaacgtctttg 1105
           ||||||||||||||||| ||  |||| |||||||| |||  |||||||||||| || ||
Db      58 GAACTCACTGGAGAAGATATCAATTCCCTCAATCCCGAAAATGAAAGCTCAACATCTGTG 117

Qy    1106 gattcaaatagcagtcaagatttggttggtggggctgttccagtccagtctcattctgaa 1165
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Db     118 GATTCCAATGGTGGTCAGGATCTGGCTGGGGCAGCTGCTCCAGATTCTTCTGGAGATTTT 177

Qy    1166 aactttacagcagctactgatttatctagatataacaacacactggtagaatcagcatca 1225
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Db    178 CAAGAAAATACTGACTCACCTAGATATGGTGACGCCGATACGGTCTGGGAGCAAACCCTA 237

Qy   1226 actcaggatgcactaactatgagaagccagctagatcaggagagtggcgctgtcatccac 1285
          |||||||||| | ||  |    ||||      |    |||     | |    | |  |
Db    238 GCTCAGGATGCTCAAAGGACTCCAAGCAGAGAGGGCTGGGAAGCCAGTGAAAACCTGAAT 297

Qy   1286 ccagccactcagacgtccctccagg 1310
          | |||||||    ||  || ||||||
Db    298 CTAGCCACGTCCACAGCCTTCCAGG 322


RESULT  12
X24979
ID   X24979 standard; cDNA; 791 BP.
AC   X24979;
DT   05-JUL-1999  (first entry)
DE   Clone GJ156 encoding TRAIN-R secreted form C-terminus.
KW   TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW   agonist; antagonist; cancer; immunological disease; therapy;
KW   cytostatic; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   intron          1. .350
FT                   /*tag= a
FT   exon            351. .790
FT                   /*tag= b
FT   CDS             352. .444
FT                   /*tag= c
FT                   /partial
FT                   /product= "TRAIN-R secreted form C-terminus"
FT   3'UTR           45. .790
FT                   /*tag= d
PN   WO9913078-A1.
PD   18-MAR-1999.
PF   11-SEP-1998; U19030.
PR   06-MAY-1998; US-084422.
PR   12-SEP-1997; US-058631.
PA   (BIOJ ) BIOGEN INC.
PI   Hession C, Tschopp J;
DR   WPI; 99-229238/19.
DR   P-PSDB; W98147.
PT   New cysteine-rich tumor necrosis factor receptor
PS   Claim 1; Page 28; 30pp; English.
CC   The present sequence includes an exon encoding the C-terminus (see
CC   W98147) of a soluble form of a novel human cysteine-rich tumour
CC   necrosis factor receptor family member termed TRAIN-R.  It comprises
CC   clone GJ156, obtained from a Clontech human adult lung cDNA library.
CC   The encoded 30-amino acid C-terminal peptide is identical to amino
CC   acids 121-149 of the composite TRAIN-R protein given in W98146 and
CC   to amino acids 121-150 of the C-terminus of murine TRAIN-R short
CC   form (secreted protein, see W98144).  The soluble protein is
CC   expected to inhibit signalling by the full-length TRAIN-R.  Human
CC   TRAIN-R is expressed at low levels in every tissue and cell line
CC   tested thus far, with higher expression detected in heart, prostate,
CC   ovary, testis, peripheral blood lymphocytes, thyroid and adrenal
CC   gland.  Cell death can be induced by administering an agent capable
CC   of inhibiting the binding of TRAIN-R to its ligand.  A claimed method
CC   of treating, or reducing, the advancement, severity or effects of
CC   an immunological disease in a mammal comprises administering a
CC   pharmaceutical composition which comprises a TRAIN-R blocking agent,
CC   e.g. soluble TRAIN-R.  TRAIN-R can be fused to an immunoglobulin to
CC   produce a fusion protein which may be targeted to various sites.
CC   It can be used in binding assays, and to identify antagonists and
CC   agonists.  Anti-TRAIN-R antibodies can be used to reduce the
CC   severity of an immune response or to treat cancer.  TRAIN-R
CC   blocking agents can also be used to reduce the severity or effects
CC   of an immunological disease (all claimed).
SQ   Sequence   791 BP;    202 A;    189 C;    165 G;    235 T;


  Query Match             6.1%;  Score 90.4;  DB 1;  Length 791;
  Best Local Similarity   89.8%;  Pred. No. 3.6e-16;
  Matches   97;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy    413 tgcttgccaggattttataggaagacgaaacttgtcggctttcaagacatggagtgtgtg 472
          | ||   |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340 TTCTCTTCTAGATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGTG 399

Qy    473 ccttgtggagaccctcctcctccttacgaaccgcactgtgccagcaag 520
          ||||||||||||||||||||||||||||||||||||||||||   | | |
Db    400 CCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGTGAGTGAACG 447


RESULT  13
V11423
ID   V11423 standard; cDNA; 181 BP.
AC   V11423;
DT   23-JUL-1998  (first entry)
DE   Human secreted protein clone AX92_3 cDNA internal fragment.
KW   Secreted protein; prevention; treatment; gene therapy; ds.
OS   Homo sapiens.
PN   WO9801554-A2.
PD   15-JAN-1998.
PF   07-JUL-1997; U11876.
PR   09-JUL-1996; US-677231.
PA   (GEMY ) GENETICS INST INC.
PI   Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM,
PI   Merberg D, Racie LA, Spaulding V, Treacy M;
DR   WPI; 98-110230/10.
DR   P-PSDB; W58844.
PT   Secreted proteins and polynucleotides encoding them - useful to
PT   prevent, treat and ameliorate medical conditions
PS   Claim 13; Page 57; 93pp; English.
CC   V11422-V11424 encode fragments of a novel secreted protein derived from
CC   clone AX92_3 which was isolated from a human fetal brain cDNA library.
CC   The protein can be used to prevent, treat or ameliorate a medical
CC   condition, while the polynucleotides can be used for gene therapy.
SQ   Sequence   181 BP;    43 A;    47 C;    34 G;    57 T;


  Query Match             5.9%;  Score 87.4;  DB 1;  Length 181;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-15;
  Matches   88;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    423 gattttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggag 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 GATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAG 147

Qy    483 accctcctcctccttacgaaccgcactgt 511
          |||||||||||||||||||||||||||| |
Db    148 ACCCTCCTCCTCCTTACGAACCGCACTCT 176


RESULT  14
V86655
ID   V86655 standard; cDNA; 201 BP.
AC   V86655;
DT   27-APR-1999  (first entry)
DE   EST clone AX92.
KW   Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW   tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW   chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW   receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
OS   Homo sapiens.
PN   WO9845435-A2.
PD   15-OCT-1998.
PF   10-APR-1998; U06954.
PR   10-APR-1997; US-835913.
PA   (GEMY ) GENETICS INST INC.
PI   Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
PI   Racie LA, Spaulding V, Treacy M;
DR   WPI; 99-070076/06.
PT   New polynucleotides encoding human secreted proteins - derived from
PT   e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT   ovary, pituitary, retina and colon cDNA libraries
PS   Claim 1; Page 306; 633pp; English.
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CC   This sequence represents an expressed sequence tag (EST), and is a
CC   polynucleotide of the invention. The polynucleotides of the invention are
CC   all secreted EST sequences isolated from a variety of human tissue
CC   sources. The EST sequences and proteins encoded by them are predicted to
CC   have useful biological activities which would make them suitable for
CC   treating, preventing or ameliorating medical conditions in humans and
CC   animals, although no supporting data is given. Suggested activities
CC   include nutritional activity, immune stimulating or suppressing activity,
CC   haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC   activity. The EST sequences are also stated to be useful for gene
CC   therapy.
SQ   Sequence   201 BP;    52 A;    51 C;    38 G;    60 T;


  Query Match             5.9%;  Score 87.4;  DB 1;  Length 201;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-15;
  Matches   88;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    423 gattttataggaagacgaaacttgtcggctttcaagacatggagtgtgtgccttgtggag 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     93 GATTTTATAGGAAGACGAAACTTGTCGGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAG 152

Qy    483 accctcctcctccttacgaaccgcactgt 511
          |||||||||||||||||||||||||||| |
Db    153 ACCCTCCTCCTCCTTACGAACCGCACTCT 181


RESULT  15
X23418
ID   X23418 standard; DNA; 396 BP.
AC   X23418;
DT   18-JUN-1999  (first entry)
DE   Mouse mAPO4-beta DNA.
KW   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW   developmental abnormality; gestational abnormalitity; prostate cancer;
KW   APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW   cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW   apoptosis; mouse; APO4-beta; ss.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   CDS             1. .289
FT                   /*tag= a
FT                   /product= "mAPO4-beta"
PN   WO9911791-A2.
PD   11-MAR-1999.
PF   04-SEP-1998; U18393.
PR   05-SEP-1997; US-924634.
PA   (UNIW ) UNIV WASHINGTON.
PI   Chaudhary PM;
DR   WPI; 99-205191/17.
DR   P-PSDB; W93584.
PT   New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT   useful for diagnosis and treatment of prostate cancer and
PT   developmental or gestational abnormalities
PS   Example IV; Fig 8; 156pp; English.
CC   This invention describes isolated Tumor Necrosis Factor (TNF) family
CC   receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC   fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC   their active fragments. APO4 is useful for diagnosing prostate cancer
CC   by determining levels of APO4 in an individual. Prostate cancer can also
CC   be treated using APO4 selective binding agents linked to a therapeutic
CC   moiety. APO4 polypeptides are also useful for identifying selective
CC   binding agents, useful in diagnosis/treatment of disease by binding of
CC   agents to the polypeptide/active fragment which is extracellular, or
CC   expressed on the cell surface. The binding is preferably performed in
CC   vivo. APO4 polypeptides/ active fragments are also useful for screening
CC   for agonists and antagonists by binding and observing the changer in APO4
CC   activity. Effective pharmacological agents useful in diagnosis or
CC   treatment of disease are also identified using APO4 polypeptides/active
CC   fragments and APO4 signal transducer molecules that specifically interact
CC   with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC   activity. The method is performed in vivo or in vitro. APO polypeptides
CC   are all useful as immunogens for preparing antibodies. APO4 is also
CC   useful for diagnosis/treatment of developmental or gestational
CC   abnormalities. APO8 was transfected to human breast carcinoma cell line
CC   MCF-7, and induced apoptosis.
SQ   Sequence   396 BP;    107 A;    102 C;    108 G;    79 T;


  Query Match             5.4%;  Score 80.4;  DB 1;  Length 396;
  Best Local Similarity   55.8%;  Pred. No. 1.7e-13;
  Matches  153;  Conservative    0;  Mismatches  121;  Indels    0;  Gaps    0;

Qy   1037 tcttatcctgaactcactggagaagacattcattctctcaatccagaacttgaaagctca 1096
          ||  |||||||||||||||||||||| |   |||| |||||||| |||   |||||| ||
Db      8 TCCGATCCTGAACTCACTGGAGAAGATACCAATTCCCTCAATCCCGAAAACGAAAGCGCA 67

Qy   1097 acgtctttggattcaaatagcagtcaagatttggttggtggggctgttccagtccagtct 1156
          | ||| ||||||| | | || | || ||| ||| |||    |||| || ||     |||
Db     68 GCATCTCTGGATTCCAGTGGCGGCCAGGATCTGGCTGGGACAGCTGCTCTAGAGTCTTCT 127

Qy   1157 cattctgaaaactttacagcagctactgatttatctagatataacaacacactggtagaa 1216
               ||          |  | |  |   |  |  |  |  |  |      ||| |    ||
Db    128 GGGAATGTTTCAGAATCTACTGACTCACCTAGACATGGTGACACTGGTACAGTCTGGGAG 187

Qy   1217 tcagcatcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgct 1276
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Db    188 CAGACGCTAGCTCAGGATGCTCAAAGGACTCCAAGCCAAGGAGGCTGGGAAGACAGGGAA 247

Qy   1277 gtcatccacccagccactcagacgtccctccagg 1310
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Db    248 AACCTGAATCTAGCCATGCCCACAGCCTTCCAGG 281


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: April 23, 2000, 01:28:55 ; Search time 700.48 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 821193 seqs, -1518192014 residues

Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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8: gb_pl2:*
9: gb_pr1:*
10: gb_pr2:*
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13: gb_sts:*
14: gb_sy:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	41.2	2.8	26258	34	CELZK816	U41018 Caenorhabdi
c 2	40.8	2.7	123416	33	AC004847	AC004847 Homo sapi
c 3	40.6	2.7	149	5	A08919	A08919 H.sapiens (
4	40.4	2.7	207699	42	AC012074	AC012074 Homo sapi
c 5	40.4	2.7	215566	42	AC012365	AC012365 Homo sapi
c 6	40.2	2.7	111944	32	HSDJ130E4	AL078582 Homo sapi
7	40.2	2.7	237316	42	AC011599	AC011599 Homo sapi
8	40	2.7	3417	7	LEGFRPOL	X80908 L.esculentu
9	40	2.7	173767	10	AC002449	AC002449 Human PAC
10	39.8	2.7	2670	7	D88490	D88490 Candida alb
11	39.6	2.7	4673	34	PFASSA	M84732 Plasmodium
c 12	39.6	2.7	299820	33	AC006803	AC006803 Caenorhab
c 13	39.6	2.7	299820	33	AC006871	AC006871 Caenorhab
14	39.4	2.6	1840	34	DDU73686	U73686 Dictyosteli
c 15	39.4	2.6	80331	40	AC004994	AC004994 Homo sapi
16	39.4	2.6	98864	11	HS460D19	AL031905 Human DNA
17	39.4	2.6	110000	32	CEY73F8_2	Continuation (3 of
18	39.4	2.6	216625	43	AC012671	AC012671 Homo sapi
19	39.4	2.6	322774	34	CEY73F8A	AL132862 Caenorhab
20	39.2	2.6	720	8	CNS01BX6	AL114802 Botrytis
21	39.2	2.6	38532	1	SCE94	AL049628 Streptomy
22	39.2	2.6	184811	43	AC009399	AC009399 Homo sapi
c 23	39.2	2.6	321003	32	PFMAL4P3	AL035476 Plasmodiu
24	39	2.6	8586	43	AC015290	AC015290 Drosophil
25	38.8	2.6	2271	10	HSM800417	AL050106 Homo sapi
c 26	38.6	2.6	1582	5	A77033	A77033 Sequence 10
c 27	38.6	2.6	1582	5	A77035	A77035 Sequence 12
28	38.6	2.6	114467	10	AP000462	AP000462 Homo sapi
c 29	38.6	2.6	128537	33	AC007775	AC007775 Homo sapi
c 30	38.4	2.6	157825	10	CNS01DRI	AL117258 Human chr
31	38.4	2.6	196287	10	CNS0000B	AL049829 Human chr
32	38.4	2.6	200509	33	AC006910	AC006910 Caenorhab
c 33	38.4	2.6	207370	33	AC006798	AC006798 Caenorhab
34	38.2	2.6	163612	43	AC012213	AC012213 Homo sapi
c 35	38.2	2.6	178972	44	AC016369	AC016369 Homo sapi
36	38.2	2.6	182374	44	AC008114	AC008114 Homo sapi
c 37	38.2	2.6	204652	32	PFMAL13P6	AL049183 Plasmodiu
c 38	38	2.6	14433	35	AE001369	AE001369 Plasmodiu
39	38	2.6	58516	42	AC011982	AC011982 Homo sapi
c 40	38	2.6	173648	43	AC015861	AC015861 Homo sapi
c 41	38	2.6	196149	33	AC004709	AC004709 Plasmodiu
42	38	2.6	208807	41	AC004688	AC004688 Plasmodiu
c 43	38	2.6	259474	40	HUAC004605	AC004605 Homo sapi
c 44	37.8	2.5	31950	34	CEC38H2	Z35641 Caenorhabdi
45	37.8	2.5	52238	33	AC007972	AC007972 Homo sapi

ALIGNMENTS

RESULT 1
CELZK816/c
LOCUS CELZK816 26258 bp DNA INV 30-NOV-1995
DEFINITION Caenorhabditis elegans cosmid ZK816.
ACCESSION U41018
VERSION U41018.1 GI:1086666
KEYWORDS .

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SOURCE      Caenorhabditis elegans strain=Bristol N2.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 26258)
  AUTHORS   Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
            Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
            Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
            Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
            Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
            Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
            O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
            Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
            Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
            Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
            Wilkinson-Sproat,J. and Wohldman,P.
  TITLE     2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
            elegans
  JOURNAL   Nature 368 (6466), 32-38 (1994)
  MEDLINE   94150718
REFERENCE   2  (bases 1 to 26258)
  AUTHORS   Nhan,M and Le,T.
  TITLE     The sequence of C. elegans cosmid ZK816
  JOURNAL   Unpublished (1995)
REFERENCE   3  (bases 1 to 26258)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-NOV-1995) Robert Waterston
COMMENT               Submitted by:
                      Genome Sequencing Center
                      Department of Genetics, Washington University,
                      St. Louis, MO  63110, USA, and
                      Sanger Centre, Hinxton Hall
                      Cambridge CB10 IRQ, England
                      e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
                      NEIGHBORING COSMID INFORMATION:
            The 5' cosmid is F11D5, 200 bp overlap; 3' cosmid is ZK563, 200 bp
            overlap. Actual start of this cosmid is at base position 35525 of
            CELF11D5; actual end is at 6673 of CELZK563.

            NOTES:
            Coding sequences below are predicted from computer analysis, using
            the program Genefinder(P. Green and L. Hillier, ms in preparation).
FEATURES              Location/Qualifiers
     source           1. .26258
                      /organism="Caenorhabditis elegans"
                      /db_xref="taxon:6239"
                      /map="X"
     gene             3410. .5744
                      /gene="ZK816.2"
     CDS              join(3410. .3500,3603. .3943,4004. .4066,4112. .4198,
                      5004. .5219,5269. .5485,5624. .5681,5729. .5744)
                      /gene="ZK816.2"
                      /note="coded for by C. elegans cDNA yk56g6.5; coded for by
                      C. elegans cDNA yk123g1.5; coded for by C. elegans cDNA
                      yk123g1.3; coded for by C. elegans cDNA yk56g6.3;  similar
                      to S. cerevisiae phosphate system positive regulatory
                      protein PHO4 (SP:PHO4_YEAST, P07270)"
                      /codon_start=1
                      /protein_id="AAA82323.1"
                      /db_xref="GI:1086667"
                      /translation="MLYSRYTNPPPTSTGCSSFQMRWVSSALRTYDKTDETTTDSMRS
                      TAPLKPPITYSPSYTSTSLNSVSLSSKYVEEKSKTSQGSTAPVVPSNSLSGLLSPREK
                      PYGDDVTILKSVSERVPENFELRRKQQVKALFRIHGRCLKFAEPTNETQKLAEPSATN
                      IVNQQDESDDNSDGDSRDGNDSYDITPMRPNSLVFTRLANEEEMGGDGNVISRSLLSL
                      VAEEDLPDFLVALNEKPIRYVVVEESEKPSTSSILRSRDARKEEKVQKGSTRIRFCTD
                      NAMAYAYLDEITATRSLQWDDGTVIEYSYFKDLEAAEEAAMAHNDPTLALIEQWEQQI
                      ANDNIHPLTHDLTFSDSCLETSAVSSAY"
     gene             7063. .7361
                      /gene="ZK816.3"
     CDS              join(7063. .7064,7110. .7175,7229. .7361)
                      /gene="ZK816.3"
                      /codon_start=1
                      /evidence=not_experimental
                      /protein_id="AAA82324.1"
                      /db_xref="GI:1086668"
                      /translation="MNASQQRPLPFFFRLFIGPHIARYLRMRRLMNEARRQNLMAHRR
                      QDNANTSSNSSVVQRSSVSETY"
     gene             complement(8331. .9120)
                      /gene="ZK816.4"
     CDS              complement(join(8331. .8479,8533. .8660,8711. .8827,
                      8878. .8954,9001. .9120))
                      /gene="ZK816.4"
                      /codon_start=1
                      /evidence=not_experimental
                      /protein_id="AAA82325.1"
                      /db_xref="GI:1086669"
                      /translation="MLAKNCILMLISLSCYYCQFKFPPPTQEFLDRSNGFYDYNSEEN
                      FERPLNASMYQPTTCGEVEQEKVKECADPLYKMGAISENSHYLGWEGFIFRTKAYFSE
                      VCDNFFLFDVCIEPYKDVCFAADRARFNYDAAIKILDFLCRDGYGEMLRNIECFTKTL
                      TRSEMMQCQAELVSDTRKISESHSEVKGANDAAVCG"
     gene             17796. .19067
                      /gene="ZK816.1"
     CDS              join(17796. .17890,18804. .18878,18923. .19067)
                      /gene="ZK816.1"
                      /codon_start=1
                      /evidence=not_experimental
                      /protein_id="AAA82326.1"
                      /db_xref="GI:1086670"
                      /translation="MWLVILCFVLPAIIFFVFALIAWLRVLQLNYRRRRATEAADREA
                      KKKASQLESLITKKDGKVICHIPIQVEDIETGAMFLYNSDENLAIIGEDAKIPLVEQQ
                      LV"
     gene             complement(19490. .21064)
                      /gene="ZK816.5"
     CDS              complement(join(19490. .19629,20019. .20172,20221. .20395,
                      20447. .20622,20699. .20961,20995. .21064))
                      /gene="ZK816.5"
                      /note="coded for by C. elegans cDNA yk102d10.5;  Similar
                      to short-chain alcohol dehydrogenase."
                      /codon_start=1
                      /protein_id="AAA82327.1"
                      /db_xref="GI:1086671"
                      /translation="MSLKSKIAIVTGASRGCGRGMLKGVALQLAEAGCTLYITGRAPS
                      KTLSSELTYLPTLEGTAEECRKRGGICHVRYVDHSNMDEVEKFFDEVASETDNQLDIL
                      VNNAFSAVTKCGSGDTRKFFERDPEIWDDINNVGLRNQYYCSVYGTRIMRKNGMKGLI
                      VNISSLGGIMYLFTVAYGVGKMALDRMSSDMAQELQDTGITVISLWPSAVKTELITNM
                      IETSAGSWGATENKMFLNGESTEYCGKAVVAIAADPKKKYWNGSTLITTDMGNYYSYT
                      DIDGRIPTNMRQLRGLLSLAGYHSMAGWCPEWVNLPGWAITLWQNKIHY"
BASE COUNT     8375 a   4735 c   4187 g   8961 t
ORIGIN


  Query Match             2.8%;  Score 41.2;  DB 34;  Length 26258;
  Best Local Similarity   67.4%;  Pred. No. 9.2;
  Matches   58;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy   1400 atgagttttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaa 1459
           || |||| |||||||||| || | |   |  ||  |  |||||||  | | ||| ||||| ||
Db   4311 ATTAGTTATTTTTTTTGGATGTATTTTTTTTGTTACTATGTTCCAAATTATTTTTTATAA 4252

Qy   1460 taaatttcaagtatttttttaaaaaa 1485
          | |||||  ||   ||  ||| | |||
Db   4251 TGAATTTTAACATTTCATTTTACAAA 4226


RESULT   2
AC004847/c
LOCUS       AC004847   123416 bp    DNA             HTG       12-JUN-1998
DEFINITION  Homo sapiens clone DJ0647J21, *** SEQUENCING IN PROGRESS ***, 10
            unordered pieces.
ACCESSION   AC004847
VERSION     AC004847.1  GI:3213150
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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           Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 123416)
  AUTHORS  Waterston,R.H.
  TITLE    The sequence of Homo sapiens clone
  JOURNAL  Unpublished
REFERENCE  2  (bases 1 to 123416)
  AUTHORS  Waterston,R.H.
  TITLE    Direct Submission
  JOURNAL  Submitted (12-JUN-1998) Genome Sequencing Center, Washington
           University School of Medicine, 4444 Forest Park Parkway, St. Louis,
           MO 63108, USA
COMMENT    * NOTE: This is a 'working draft' sequence. It currently
           * consists of 10 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           *        1     1580: contig of 1580 bp in length
           *     1581     1598: gap of unknown length
           *     1599     3512: contig of 1914 bp in length
           *     3513     3530: gap of unknown length
           *     3531     6664: contig of 3134 bp in length
           *     6665     6682: gap of unknown length
           *     6683    11088: contig of 4406 bp in length
           *    11089    11106: gap of unknown length
           *    11107    20349: contig of 9243 bp in length
           *    20350    20367: gap of unknown length
           *    20368    33197: contig of 12830 bp in length
           *    33198    33215: gap of unknown length
           *    33216    43072: contig of 9857 bp in length
           *    43073    43090: gap of unknown length
           *    43091    65746: contig of 22656 bp in length
           *    65747    65764: gap of unknown length
           *    65765    85268: contig of 19504 bp in length
           *    85269    85286: gap of unknown length
           *    85287   123416: contig of 38130 bp in length.
FEATURES             Location/Qualifiers
     source          1. .123416
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DJ0647J21"
BASE COUNT    30903 a  29142 c  29866 g  33343 t    162 others
ORIGIN
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  Best Local Similarity   59.5%;  Pred. No. 14;
  Matches   69;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy   1365 actctgttcccagcataagatttgggggaacctggatgagtttttttttttgcatcttta 1424
          |||||||||  |    | ||  ||  |  |         ||| || |||||  || ||||
Db  34675 ACTCTGTTCAGATGGCAGGACATGAAGTCAAAGAAGATTGTTCTTCTTTTTTAATTTTTA 34616

Qy   1425 ataatttcttatatgttgtagagtatgttttaaaataaatttcaagtatttttttta 1480
          | || |  || ||  || || | |   |||| |  |||| || | |||||| ||||
Db  34615 AAAAATATTTTTAAATTATACATTTATTTTTTACTTAAAATTTACGTATTTATTTA 34560


RESULT   3
A08919/c
LOCUS       A08919        149 bp    DNA             PAT       02-SEP-1993
DEFINITION  H.sapiens (haplotype 2A, allele MS32, isolate English, serial
            number 30) minisatellite sequence.
ACCESSION   A08919
VERSION     A08919.1  GI:411841
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 149)
  AUTHORS   Jeffreys,A.J.
  TITLE     Extended nucleotide sequences
  JOURNAL   Patent: EP 0370719-A 74 30-MAY-1990;
            IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES             Location/Qualifiers
     source          1. .149
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      100 a      0 c      0 g     49 t
ORIGIN
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  Query Match             2.7%;  Score 40.6;  DB 5;  Length 149;
  Best Local Similarity   66.7%;  Pred. No. 6.9;
  Matches   58;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy   1403 agttttttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataa 1462
          | ||||||||||||   | ||||||  ||| || ||| || || | | |  |||      |
Db     92 ATTTTTTTTTTTTTTTTTTTAATTTTTTTTTTTATTTTTTATAATTTTATTTTTTTATA 33

Qy   1463 atttcaagtatttttttaaaaaacttt 1489
          |||| |  | |||||||| ||| | |
Db     32 ATTTTATTTTTTTTTTTAATAAAATAT 6


RESULT   4
AC012074
LOCUS       AC012074   207699 bp    DNA             HTG       19-OCT-1999
DEFINITION  Homo sapiens clone NH0458N05, *** SEQUENCING IN PROGRESS ***, 40
            unordered pieces.
ACCESSION   AC012074
VERSION     AC012074.1  GI:6067201
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 207699)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 207699)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-OCT-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 40 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2641: contig of 2641 bp in length
            *     2642     2660: gap of unknown length
            *     2661     5448: contig of 2788 bp in length
            *     5449     5467: gap of unknown length
            *     5468     9447: contig of 3980 bp in length
            *     9448     9466: gap of unknown length
            *     9467    13258: contig of 3792 bp in length
            *    13259    13277: gap of unknown length
            *    13278    17777: contig of 4500 bp in length
            *    17778    17796: gap of unknown length
            *    17797    22203: contig of 4407 bp in length
            *    22204    22222: gap of unknown length
            *    22223    25932: contig of 3710 bp in length
            *    25933    25951: gap of unknown length
            *    25952    29791: contig of 3840 bp in length
            *    29792    29810: gap of unknown length
            *    29811    33884: contig of 4074 bp in length
            *    33885    33903: gap of unknown length
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            *    33904    38171: contig of 4268 bp in length
            *    38172    38190: gap of unknown length
            *    38191    43737: contig of 5547 bp in length
            *    43738    43756: gap of unknown length
            *    43757    48978: contig of 5222 bp in length
            *    48979    48997: gap of unknown length
            *    48998    56306: contig of 7309 bp in length
            *    56307    56325: gap of unknown length
            *    56326    63986: contig of 7661 bp in length
            *    63987    64005: gap of unknown length
            *    64006    70568: contig of 6563 bp in length
            *    70569    70587: gap of unknown length
            *    70588    76401: contig of 5814 bp in length
            *    76402    76420: gap of unknown length
            *    76421    86970: contig of 10550 bp in length
            *    86971    86989: gap of unknown length
            *    86990    98169: contig of 11180 bp in length
            *    98170    98188: gap of unknown length
            *    98189   108152: contig of 9964 bp in length
            *   108153   108171: gap of unknown length
            *   108172   119388: contig of 11217 bp in length
            *   119389   119407: gap of unknown length
            *   119408   133082: contig of 13675 bp in length
            *   133083   133101: gap of unknown length
            *   133102   146342: contig of 13241 bp in length
            *   146343   146361: gap of unknown length
            *   146362   164088: contig of 17727 bp in length
            *   164089   164106: gap of unknown length
            *   164107   166221: contig of 2115 bp in length
            *   166222   166239: gap of unknown length
            *   166240   168580: contig of 2341 bp in length
            *   168581   168598: gap of unknown length
            *   168599   171138: contig of 2540 bp in length
            *   171139   171156: gap of unknown length
            *   171157   173430: contig of 2274 bp in length
            *   173431   173448: gap of unknown length
            *   173449   175478: contig of 2030 bp in length
            *   175479   175496: gap of unknown length
            *   175497   177569: contig of 2073 bp in length
            *   177570   177587: gap of unknown length
            *   177588   180479: contig of 2892 bp in length
            *   180480   180497: gap of unknown length
            *   180498   182910: contig of 2413 bp in length
            *   182911   182928: gap of unknown length
            *   182929   185768: contig of 2840 bp in length
            *   185769   185786: gap of unknown length
            *   185787   188176: contig of 2390 bp in length
            *   188177   188194: gap of unknown length
            *   188195   190684: contig of 2490 bp in length
            *   190685   190702: gap of unknown length
            *   190703   194580: contig of 3878 bp in length
            *   194581   194598: gap of unknown length
            *   194599   197276: contig of 2678 bp in length
            *   197277   197294: gap of unknown length
            *   197295   199995: contig of 2701 bp in length
            *   199996   200013: gap of unknown length
            *   200014   202982: contig of 2969 bp in length
            *   202983   203000: gap of unknown length
            *   203001   205501: contig of 2501 bp in length
            *   205502   205519: gap of unknown length
            *   205520   207699: contig of 2180 bp in length.
FEATURES             Location/Qualifiers
     source          1. .207699
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="NH0458N05"
BASE COUNT    61977 a  41162 c  41291 g  62545 t    724 others
ORIGIN


  Query Match             2.7%;  Score 40.4;  DB 42;  Length 207699;
  Best Local Similarity   65.6%;  Pred. No. 19;
  Matches   59;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy   1395 cctggatgagttttttttttgcatctttaataatttcttatatgttgtagagtatgttt 1454
           | ||| | | ||| || ||||  | || ||||  | |   || || | |||| |||  |
Db 127387 CGTGGCTTATTTTATTATTTTTAAACTATAATCTTCTGGAATTTGCTTTAGAATATTATG 127446

Qy   1455 taaaataaatttcaagtatttttttaaaaa 1484
           |||||  ||| | || |||| |||| | ||
Db 127447 TAAAAATAATGTAAATTATTATTTTTATAA 127476


RESULT   5
AC012365/c
LOCUS       AC012365   215566 bp    DNA             HTG       25-OCT-1999
DEFINITION  Homo sapiens clone NH0459C22, *** SEQUENCING IN PROGRESS ***, 37
            unordered pieces.
ACCESSION   AC012365
VERSION     AC012365.1  GI:6114946
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 215566)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 215566)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 37 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     6252: contig of 6252 bp in length
            *    6253     6271: gap of unknown length
            *    6272    13316: contig of 7045 bp in length
            *   13317    13335: gap of unknown length
            *   13336    21229: contig of 7894 bp in length
            *   21230    21248: gap of unknown length
            *   21249    27594: contig of 6346 bp in length
            *   27595    27613: gap of unknown length
            *   27614    35972: contig of 8359 bp in length
            *   35973    35991: gap of unknown length
            *   35992    45671: contig of 9680 bp in length
            *   45672    45690: gap of unknown length
            *   45691    58710: contig of 13020 bp in length
            *   58711    58729: gap of unknown length
            *   58730    71377: contig of 12648 bp in length
            *   71378    71396: gap of unknown length
            *   71397    90008: contig of 18612 bp in length
            *   90009    90027: gap of unknown length
            *   90028   121592: contig of 31565 bp in length
            *  121593   121610: gap of unknown length
            *  121611   124080: contig of 2470 bp in length
            *  124081   124098: gap of unknown length
            *  124099   126360: contig of 2262 bp in length
            *  126361   126378: gap of unknown length
            *  126379   129231: contig of 2853 bp in length
            *  129232   129249: gap of unknown length
            *  129250   131412: contig of 2163 bp in length
            *  131413   131430: gap of unknown length
            *  131431   134035: contig of 2605 bp in length
            *  134036   134053: gap of unknown length
            *  134054   136191: contig of 2138 bp in length
            *  136192   136209: gap of unknown length
            *  136210   138604: contig of 2395 bp in length
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            *   138605   138622: gap of unknown length
            *   138623   141375: contig of 2753 bp in length
            *   141376   141393: gap of unknown length
            *   141394   144063: contig of 2670 bp in length
            *   144064   144081: gap of unknown length
            *   144082   146269: contig of 2188 bp in length
            *   146270   146287: gap of unknown length
            *   146288   149382: contig of 3095 bp in length
            *   149383   149400: gap of unknown length
            *   149401   152120: contig of 2720 bp in length
            *   152121   152138: gap of unknown length
            *   152139   155611: contig of 3473 bp in length
            *   155612   155629: gap of unknown length
            *   155630   157629: contig of 2000 bp in length
            *   157630   157647: gap of unknown length
            *   157648   162928: contig of 5281 bp in length
            *   162929   162946: gap of unknown length
            *   162947   165662: contig of 2716 bp in length
            *   165663   165680: gap of unknown length
            *   165681   168902: contig of 3222 bp in length
            *   168903   168920: gap of unknown length
            *   168921   171775: contig of 2855 bp in length
            *   171776   171793: gap of unknown length
            *   171794   175625: contig of 3832 bp in length
            *   175626   175643: gap of unknown length
            *   175644   179540: contig of 3897 bp in length
            *   179541   179558: gap of unknown length
            *   179559   183777: contig of 4219 bp in length
            *   183778   183795: gap of unknown length
            *   183796   187401: contig of 3606 bp in length
            *   187402   187419: gap of unknown length
            *   187420   192407: contig of 4988 bp in length
            *   192408   192425: gap of unknown length
            *   192426   197395: contig of 4970 bp in length
            *   197396   197413: gap of unknown length
            *   197414   203803: contig of 6390 bp in length
            *   203804   203821: gap of unknown length
            *   203822   209450: contig of 5629 bp in length
            *   209451   209468: gap of unknown length
            *   209469   215566: contig of 6098 bp in length.
FEATURES             Location/Qualifiers
     source          1. .215566
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="NH0459C22"
BASE COUNT    55527 a  52861 c  53096 g  53425 t    657 others
ORIGIN


  Query Match             2.7%;  Score 40.4;  DB 42;  Length 215566;
  Best Local Similarity   65.6%;  Pred. No. 19;
  Matches   59;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy   1395 cctggatgagttttttttttttgcatctttaataatttcttatatgttgtagagtatgtttt 1454
           | ||| | | ||| || ||||  | || ||||  | |   || || | |||| |||  |
Db 124819 CGTGGCTTATTTTATTATTTTTAAACTATAATCTTCTGGAATTTGCTTTAGAATATTATG 124760

Qy   1455 taaaataaatttcaagtatttttttaaaaa 1484
          |||||  ||| | || |||| |||| | ||
Db 124759 TAAAAATAATGTAAATTATTATTTTTATAA 124730


RESULT   6
HSDJ130E4/c
LOCUS       HSDJ130E4  111944 bp    DNA             HTG       23-NOV-1999
DEFINITION  Homo sapiens chromosome 6 clone RP1-130E4, *** SEQUENCING IN
            PROGRESS ***, in unordered pieces.
ACCESSION   AL078582
VERSION     AL078582.7  GI:6018773
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 111944)
  AUTHORS   Parker,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-NOV-1999) Wellcome Trust Genome Campus, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquires:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Oct 11, 1999 this sequence version replaced gi:6018475.
            IMPORTANT: This sequence is unfinished and does not necessarily
            represent the correct sequence. Work on the sequence is in progress
            and the release of this data is based on the understanding that the
            sequence may change as work continues. The sequence may be
            contaminated with foreign sequence from E.coli, yeast, vector,
            phage etc. Order of segments is not known; 800 n's separate
            segments. Unfinished: dJ130E4  Contig_ID: 00522  acc=AL078582
            Length: 111944 bp.
            * NOTE: This is a 'working draft' sequence.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
FEATURES             Location/Qualifiers
     source          1. .111944
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="RP1-130E4"
                     /clone_lib="RPCI-1"
BASE COUNT    33294 a  23483 c  22954 g  32213 t
ORIGIN


  Query Match             2.7%;  Score 40.2;  DB 32;  Length 111944;
  Best Local Similarity   67.1%;  Pred. No. 19;
  Matches   57;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy   1405 ttttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataaat 1464
           || | ||| ||  |   ||||| |||  | |||   |  | | ||| | || ||||||||
Db  40544 TTATATTTATTTAAATATTAATTATTAATAATAAAATAAATATTATTTATTTAAATAAAT 40485

Qy   1465 ttcaagtatttttttaaaaaacttt 1489
           | ||||||| ||||||  |  |||
Db  40484 ATTAAGTATTTATTTAAATACATTT 40460


RESULT   7
AC011599
LOCUS       AC011599   237316 bp    DNA             HTG       21-OCT-1999
DEFINITION  Homo sapiens chromosome 3 seeders clone RPCI11-606L6, ***
            SEQUENCING IN PROGRESS ***, 29 unordered pieces.
ACCESSION   AC011599
VERSION     AC011599.2  GI:6087865
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 237316)
  AUTHORS   Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K.,
            Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C.,
            Burkett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,
            David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
            Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
            Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L.,
            Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
            Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,
            Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,
            Lichtarge,O., Liu,J., Liu,W., Logan,O., Lu,J., Lucier,R.,
            Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M., Morris,S.,
            Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G.,
            Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M.,
            Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E.,
            Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R., Tabor,P.,
            Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S.,
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            Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Wren,J.,
            Wrensford,G., Yu,W., Zhou,X., Nelson,D. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 237316)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Oct 20, 1999 this sequence version replaced gi:6016622.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 29 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *         1      1094: contig of 1094 bp in length
            *      1095      1961: contig of 867 bp in length
            *      1962      3033: contig of 1072 bp in length
            *      3034      3849: contig of 816 bp in length
            *      3850      4810: contig of 961 bp in length
            *      4811      5605: contig of 795 bp in length
            *      5606      6754: contig of 1149 bp in length
            *      6755      7721: contig of 967 bp in length
            *      7722      8612: contig of 891 bp in length
            *      8613      9661: contig of 1049 bp in length
            *      9662     10580: contig of 919 bp in length
            *     10581     11501: contig of 921 bp in length
            *     11502     12914: contig of 1413 bp in length
            *     12915     13809: contig of 895 bp in length
            *     13810     14625: contig of 816 bp in length
            *     14626     15624: contig of 999 bp in length
            *     15625     16672: contig of 1048 bp in length
            *     16673     17704: contig of 1032 bp in length
            *     17705     19083: contig of 1379 bp in length
            *     19084     20081: contig of 998 bp in length
            *     20082     20958: contig of 877 bp in length
            *     20959     23350: contig of 2392 bp in length
            *     23351     26220: contig of 2870 bp in length
            *     26221     32049: contig of 5829 bp in length
            *     32050     46821: contig of 14772 bp in length
            *     46822     64420: contig of 17599 bp in length
            *     64421     91572: contig of 27152 bp in length
            *     91573    129163: contig of 37591 bp in length
            *    129164    237316: contig of 108153 bp in length.
FEATURES             Location/Qualifiers
     source          1. .237316
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3 seeders"
                     /clone="RPCI11-606L6"
BASE COUNT    54463 a  63949 c  63339 g  55490 t     75 others
ORIGIN
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  Query Match             2.7%;  Score 40.2;  DB 42;  Length 237316;
  Best Local Similarity   49.8%;  Pred. No. 21;
  Matches  102;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy    746 gaatatgcccacagagcctgctgccagtgccgccgtgactcagtgcagacctgcgggccg 805
          | | || |||||   |||     ||| ||||  |   ||    |    | || | | |  |
Db  58413 GCAGATTCCCACCCCGCCCTGCCCCACTGCCCGCCCCACGGGGAAGTGGCCCGGGAGTGG 58472

Qy    806 gtgcgcttgctcccatccatgtgctgtgaggaggcctgcagccccaacccggcgactctt 865
           |||    |   |||||  |||    |||   | |||  |  |||| || ||  |
Db  58473 AGGCGTGGACAGGCATCCCGGTGTCTCGAGTCAGGCTGTCGGGCCAGCCTGGACAGCACG 58532

Qy    866 ggttgtggggtgcattctgcagccagtcttcaggcaagaaacgcaggcccagccggggag 925
          |   | || | |||  | |    ||     |||||   |  | |  |  ||||||  ||
Db  58533 GCCCGCGGAGGGCAGACAGGGCGCACGGAGCAGGCCCCAGGCTCCAGAGCAGCCGCTGAC 58592

Qy    926 atggtgccgactttcttcggatccc 950
          | | || | |  | | |||| || |
Db  58593 AGGCTGTCCAGCTGCATCGGGTCTC 58617
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```
RESULT   8
LEGFRPOL
LOCUS       LEGFRPOL     3417 bp    DNA             PLN       24-AUG-1995
DEFINITION  L.esculentum gene for fruit ripening polygalacturonase.
ACCESSION   X80908
VERSION     X80908.1  GI:963065
KEYWORDS    polygalacturonase.
SOURCE      tomato.
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
            Asteridae; Solananae; Solanales; Solanaceae; Solanum; Potatoe;
            Lycopersicon.
REFERENCE   1  (bases 1 to 3417)
  AUTHORS   Nicholass,F.J., Smith,C.J., Schuch,W., Bird,C.R. and Grierson,D.
  TITLE     High levels of ripening-specific reporter gene expression directed
            by tomato fruit polygalacturonase gene-flanking regions
  JOURNAL   Plant Mol. Biol. 28 (3), 423-435 (1995)
  MEDLINE   95359401
REFERENCE   2  (bases 1 to 3417)
  AUTHORS   Nicholass,F.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-AUG-1994) F.J. Nicholass, University of Nottingham,
            AFRC Research Group in Plant Gene Reg., Dept of Physiology & Envir.
            Science, Sutton Bonigton Campus, Loughborough Leics. LE12 5RD, UK
FEATURES             Location/Qualifiers
     source          1...3417
                     /organism="Lycopersicon esculentum"
                     /cultivar="Ailsa Craig"
                     /db_xref="taxon:4081"
                     /chromosome="10"
                     /clone="GTOM23.73"
     mRNA            1. .3417
                     /product="fruit ripening specific polygalacturonase"
BASE COUNT     1307 a    438 c    424 g   1248 t
ORIGIN
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```
  Query Match             2.7%;  Score 40;  DB 7;  Length 3417;
  Best Local Similarity   65.9%;  Pred. No. 14;
  Matches   58;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy   1400 atgagttttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaa 1459
          | || || |||||     |   || ||| ||  | |    ||  || |||| |||||||||
Db   3173 AAGAATTATTTTTGAGCAACAATTTATATTTAGTCACGCTTTTAAGTGTATTTTTTAAAA 3232

Qy   1460 taaatttcaagtatttttttaaaaaact 1487
          |||| || | ||||| ||| |||||| |
Db   3233 TAAAATTAAGGTATTATTTGAAAAATT 3260
```

```
RESULT   9
AC002449
LOCUS       AC002449   173767 bp    DNA             PRI       20-AUG-1997
DEFINITION  Human PAC clone DJ404K21 from Xq23, complete sequence.
ACCESSION   AC002449
VERSION     AC002449.1  GI:2337886
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 173767)
  AUTHORS   Hinds,K, Tin-Wollam,A, Sutterer,C and Fronick,B.
  TITLE     The sequence of H. sapiens PAC clone DJ404K21
  JOURNAL   Unpublished (1997)
REFERENCE   2  (bases 1 to 173767)
```

```
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-AUG-1997) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     SUBMITTED BY:
            Genome Sequencing Center
            Department of Genetics
            Washington University
            St. Louis MO 63108, USA
            http://genome.wustl.edu/gsc
            mailto:sapiens@watson.wustl.edu

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded or sequenced with an alternate
            chemistry; an attempt was made to resolve all sequencing problems,
            such as compressions and repeats; all regions were covered by
            sequence from more than one subclone; and the assembly was
            confirmed by restriction digest.

            MAPPING INFORMATION:
            This sequence was generated from part of bacterial clone contigs of
            human chromosome X, constructed by David Bentley's chromosome X
            mapping group at the Sanger Centre, Wellcome Trust Genome Campus,
            Hinxton, UK.  Further information can be found at
            http://www.sanger.ac.uk/HGP/ChrX

            SOURCE INFORMATION:
            This clone was derived from human PAC library RPCI-3 prepared by
            Pieter de Jong and coworkers at Roswell Park Cancer Institute,
            using the method described by Ioannou et al., Nature Genetics
            6:84-9 (1994).  The library is from one male donor.  For further
            details, see http://bacpac.med.buffalo.edu/  The clone is available
            from Genome Systems, Inc. (http://www.genomesystems.com).
            VECTOR:  pCYPAC2

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is H_DJ290B04. The actual start of
            this clone is at base position 1 of DJ404K21; actual end is at
            173767 of DJ404K21. This clone is part of an unanchored island,
            orientation is unknown.

            This clone contains STS's sWXD757 (NID:g405440) and sWXD512
            (NID:g995449).
FEATURES              Location/Qualifiers
     source           1. .173767
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /chromosome="X"
                      /clone="DJ404K21"
                      /clone_lib="RPCI-3"
                      /map="Xq23"
     repeat_region    3958. .3983
                      /rpt_family="L1"
     repeat_region    7187. .7448
                      /rpt_family="MER"
     repeat_region    7450. .7832
                      /rpt_family="ALU"
     repeat_region    complement(7833. .7891)
                      /rpt_family="THR"
     repeat_region    7893. .8184
                      /rpt_family="ALU"
     repeat_region    complement(8198. .9670)
                      /rpt_family="THR"
     repeat_region    9671. .10045
                      /rpt_family="ALU"
     repeat_region    10047. .10226
                      /rpt_family="MER"
     repeat_region    10461. .11065
                      /rpt_family="L1"
     repeat_region    complement(11071. .11286)
                      /rpt_family="MER"
     repeat_region    11291. .11433
                      /rpt_family="L1"
     repeat_region    complement(11434. .11593)
                      /rpt_family="MER"
     repeat_region    complement(11616. .11641)
                      /rpt_family="MER"
     repeat_region    complement(14472. .14820)
                      /rpt_family="L1"
     repeat_region    complement(14833. .15202)
                      /rpt_family="L1"
     repeat_region    15777. .15808
                      /rpt_family="L1"
     repeat_region    16030. .16436
                      /rpt_family="L1"
     repeat_region    16625. .16719
                      /rpt_family="L1"
     repeat_region    16860. .18448
                      /rpt_family="L1"
     repeat_region    18450. .18738
                      /rpt_family="ALU"
     repeat_region    18756. .22756
                      /rpt_family="L1"
     repeat_region    complement(24561. .24819)
                      /rpt_family="ALU"
     repeat_region    25322. .25360
                      /rpt_family="L1"
     repeat_region    25871. .25936
                      /rpt_family="L1"
     repeat_region    27205. .27559
                      /rpt_family="ALU"
     repeat_region    27921. .28394
                      /rpt_family="L1"
     repeat_region    29212. .29235
                      /rpt_family="L1"
     repeat_region    complement(30468. .30557)
                      /rpt_family="L1"
     misc_feature     30844. .31126
                      /note="match to EST R00201 (NID:g749937) ye71f11.r1"
     misc_feature     31050. .31156
                      /note="match to EST R00201 (NID:g749937) ye71f11.r1"
     repeat_region    31530. .32115
                      /rpt_family="L1"
     repeat_region    complement(34006. .34295)
                      /rpt_family="ALU"
     repeat_region    35839. .35865
                      /rpt_family="L1"
     repeat_region    36463. .37291
                      /rpt_family="L1"
     repeat_region    39129. .39159
                      /rpt_family="L1"
     repeat_region    complement(39829. .40254)
                      /rpt_family="ALU"
     repeat_region    40512. .41114
                      /rpt_family="L1"
     repeat_region    41227. .41458
                      /rpt_family="L1"
     repeat_region    complement(41461. .41750)
                      /rpt_family="ALU"
     repeat_region    42582. .42630
                      /rpt_family="L1"
     repeat_region    43534. .43661
                      /rpt_family="L1"
     repeat_region    44290. .44440
                      /rpt_family="L1"
     repeat_region    44494. .44678
                      /rpt_family="L1"
     repeat_region    complement(45130. .45422)
                      /rpt_family="ALU"
     repeat_region    complement(45972. .46009)
                      /rpt_family="THR"
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     repeat_region   47644. .47668
                     /rpt_family="L1"
     repeat_region   48498. .48788
                     /rpt_family="ALU"
     repeat_region   complement(49482. .49770)
                     /rpt_family="ALU"
     repeat_region   complement(51436. .51509)
                     /rpt_family="L1"
     repeat_region   complement(51533. .51623)
                     /rpt_family="L1"
     repeat_region   complement(52389. .52862)
                     /rpt_family="L1"
     repeat_region   complement(52874. .54009)
                     /rpt_family="L1"
     repeat_region   54033. .54244
                     /rpt_family="L1"
     repeat_region   complement(54308. .54351)
                     /rpt_family="L1"
     repeat_region   54388. .54524
                     /rpt_family="ALU"
     repeat_region   54525. .57141
                     /rpt_family="L1"
     repeat_region   57168. .58229
                     /rpt_family="L1"
     repeat_region   58231. .58520
                     /rpt_family="ALU"
     repeat_region   58522. .61300
                     /rpt_family="L1"
     repeat_region   61313. .61482
                     /rpt_family="ALU"
     repeat_region   complement(61490. .61545)
                     /rpt_family="L1"
     repeat_region   complement(61550. .61830)
                     /rpt_family="ALU"
     repeat_region   complement(61833. .61952)
                     /rpt_family="L1"
     repeat_region   63130. .63422
                     /rpt_family="ALU"
     repeat_region   complement(63435. .63457)
                     /rpt_family="MER"

  Query Match              2.7%;  Score 40;  DB 10;  Length 173767;
  Best Local Similarity   55.9%;  Pred. No. 23;
  Matches   76;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy      43 ataaatacatttgataagaaagatggctttaaaagtgctactagaacaagagaaaacgtt 102
           | |||||||||| | |||||||| ||  | | |||   |||   || || | || || ||
Db   39644 AAAAATACATTTTAAAAGAAAGAGGGGATGACAAGAAATACACTAATAATAAAAGACATT 39703

Qy     103 tttcactcttttagtattactaggctatttgtcatgtaaagtgacttgtgaatcaggaga 162
             |   ||   |   |  ||  ||  | | | || |||| |  |   | || |||   ||
Db   39704 AATTTGTCAAATTCCAAGACAGGGTGAGTAGACAAGTAAGGATATAAGAGACTCAAATGA 39763

Qy     163 ctgtagacagcaagaa 178
           |   |   |  ||| |
Db   39764 CGTAATTAATGAAGCA 39779


RESULT  10
D88490
LOCUS       D88490       2670 bp    mRNA            PLN       26-JUN-1999
DEFINITION  Candida albicans mRNA for CaKRE6, complete cds.
ACCESSION   D88490
VERSION     D88490.1  GI:1944423
KEYWORDS    CaKRE6.
SOURCE      Candida albicans cDNA to mRNA.
  ORGANISM  Candida albicans
            Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
            Candidaceae; Candida.
REFERENCE   1  (sites)
  AUTHORS   Mio,T., Yamada-Okabe,T., Yabe,T., Nakajima,T., Arisawa,M. and
            Yamada-Okabe,H.
  TITLE     Isolation of the Candida albicans homologs of Saccharomyces
            cerevisiae KRE6 and SKN1: expression and physiological function
  JOURNAL   J. Bacteriol. 179 (7), 2363-2372 (1997)
  MEDLINE   97234650
REFERENCE   2  (bases 1 to 2652)
  AUTHORS   Mio,T., Yamada-Okabe,T., Yabe,T., Nakajima,T., Arisawa,M. and
            Yamada-Okabe,H.
  TITLE     Isolation from Candida albicans of the Saccharomyces cerevisiae
            KRE6 and SKN1homologues: expression and physiological function
  JOURNAL   Unpublished (1997)
REFERENCE   3  (bases 1 to 2670)
  AUTHORS   Okabe,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1996) to the DDBJ/EMBL/GenBank databases. Toshiko
            Okabe, Yokohama City University, School of Medicine, Department of
            Hygiene; 3-9 Fukuura, Kanazawa-ku, Yokohama, Kanagawa 236-0004,
            Japan (E-mail:toshiko@med.yokohama-cu.ac.jp, Tel:81-45-787-2606,
            Fax:81-45-786-5219)
FEATURES             Location/Qualifiers
     source          1. .2670
                     /organism="Candida albicans"
                     /db_xref="taxon:5476"
     CDS             51. .2273
                     /codon_start=1
                     /transl_table=12
                     /product="CaKRE6"
                     /protein_id="BAA19593.1"
                     /db_xref="GI:1944424"
                     /translation="MASQRDLTSNNPHFHISSSRNNTNDDFNSDHNPRNPFGDEPEEE
                     EELDSASFSSSSQNNQPHHPFATSNQTSSTNNLHSTNSIRNEAEYGKPFQAYSGYYSN
                     GGSSSYLNQEGVISDESRLLSSGNNNNNNNNNRDVSSVGGGGGSGDNRLNPTSPAEFD
                     RYPSMAGSRVVSSTSLVSFNNPSNMMRNHHQHQPHLGSSSSPTSSSMNNDSISDKSTS
                     PFPNDFSPFGGYPASSFPLSIDEKEPDDYLNNPDPVQDAEYEKNRFMHDLKNMDKRSL
                     GGLIGFIILFIAALAVFIILPALTYSGATNPYHPESYEVLTKYSYPMLSAIRMNLVDP
                     DTPESAYKKKAKDGSEWVLVFSDEFDAEGRTFYEGDDQFFTAPDIHYDATKDLEWYDP
                     DAVTTANGTLNLRMDAYKNHNLFYRSGMVQSWNQLCYTQGHLEISARLPNYGNVTGLW
                     PGLWSMGNLGRPGYLGSTDGVWPYSYDSCDAGITPNQSSPDGISYLPGQRLNKCTCPG
                     ELHPNRGVGRGAPEIDVIEGEVMTDSSGKKENCGVASQSLQLAPMDIWYIPDYNWVEI
                     YNFSVSTMNTYTGGPFQQALSATTMLNVTWYEFGDNAHNFQTYGYEYLNDPETGYLRW
                     FVGDDPTLTVYSQALHPDGNIGWRPLSKEPMSLILNLGISNNWAYIDWPSISFPVTFR
                     IDYVRVYQPPDQINVGCDPTDFPTYDYIQQHLNLYENANITSFEDGGYKFPKNSLIGC
                     "
     polyA_site      2652
                     /note="18 A nucleotides"
BASE COUNT      874 a    404 c    457 g    935 t
ORIGIN


  Query Match              2.7%;  Score 39.8;  DB 7;  Length 2670;
  Best Local Similarity   67.5%;  Pred. No. 15;
  Matches   56;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy    1403 agttttttttttgcatctttaataatttcttatatgttgtagagtatgttttaaaataa 1462
           ||| |||||| ||  || || |||| | | |||| |||| |||| | | ||||||| ||
Db    2579 AGTCTTTTTTATTATATTTTAAATATTATATTATTTGTTATAGAATTTTTTTTAAATAAA 2638

Qy    1463 atttcaagtatttttttaaaaaa 1485
             ||  | |:| |    ||||||
Db    2639 GCTTTTATTTTATCAAAAAAAAA 2661


RESULT  11
PFASSA
LOCUS       PFASSA :     4673 bp    DNA             INV       26-APR-1993
DEFINITION  Plasmodium yoelii sporozoite surface protein 2 gene , complete cds.
ACCESSION   M84732
VERSION     M84732.1  GI:160692
KEYWORDS    sporozoite surface protein.
SOURCE      Plasmodium yoelii erythrocytic stage blood DNA.
  ORGANISM  Plasmodium yoelii
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 4673)
  AUTHORS   Rogers,W.O., Rogers,M.D., Hedstrom,R. and Hoffman,S.L.
  TITLE     Characterization of the gene encoding Sporozoite Surface Protein 2,
```

```
          a protective Plasmodium yoelii sporozoite antigen
  JOURNAL   Mol. Biochem. Parasitol. 53, 45-52 (1992)
  MEDLINE   92365736
FEATURES             Location/Qualifiers
     source          1. .4673
                     /organism="Plasmodium yoelii"
                     /db_xref="taxon:5861"
                     /cell_type="erythrocytic stage"
                     /dev_stage="erythrocytic stage"
                     /tissue_type="blood"
     gene            718. .3198
                     /gene="sporozoite surface protein"
     CDS             718. .3198
                     /gene="sporozoite surface protein"
                     /codon_start=1
                     /product="sporozoite surface protein"
                     /protein_id="AAA29768.1"
                     /db_xref="GI:160693"
                     /translation="MKLLGNSKYIFVVLLLCISVFLNGQETLDEIKYSEEVCTEQIDI
                     HILLDGSGSIGYSNWKAHVIPMLNTLVDNLNISNDEINVSLTLFSTNSRELIKLKGYG
                     STSKDSLRFILAHLQNNYSPNGNTNLTSALLVVDTLINERMYRPDAIQLAIILTDGIP
                     NDLPRSTAVVHQLKRKHVNVAIIGVGAGVNNEYNRILVGCDRYAPCPYYSSGSWNEAQ
                     NMIKPFLTKVCQEVERIAHCGKWEEWSECSTTCDEGRKIRRRQILHPGCVSEMTTPCK
                     VRDCPQIPIPPVIPNKIPEKPSNPEEPVNPNDPNDPNNPNNPNNPNNPNNPNNPNPN
                     NPNNPNNPNNPNNPNNPNNPNNPNNPNNPNNPNNPNNPNNPDPSNPNNHPK
                     RRNPKRRNPNKPKPNKPNPNKPNPNEPSNPNKPNPNEPSNPNKPNPNEPSNPNKPNPN
                     EPSNPNKPNPNEPLNPNEPSNPNEPSNPNAPSNPNEPSNPNEPSNPNEPSNPNEPSNP
                     NEPSNPKKPSNPNEPSNPNEPLNPNEPSNPNEPSNPNEPSNPEEPSNPKEPSNPNEPS
                     NPEEPNPEEPSNPKEPSNPEEPINPEELNPKEPSNPEESNPKEPINPEESNPKEPINP
                     EDNENPLIIQDEPIEPRNDSNVIPILPIIPQKGNNIPSNLPENPSDSEVEYPRPNDNG
                     ENSNNTMKSKKNIPNEPIPSPGDNPYKGHEERIPKPHRSNDDYVYDNNVNKNNKDEPE
                     IPNNEYEEDKNKNQSKSNNGYKIAGGIIGGLAILGCAGVGYNFIAGSSAAGLAGAEPA
                     PFEDVIPDDDKDIVENEQFKLPEDNDWN"
BASE COUNT     1836 a    807 c    530 g   1500 t
ORIGIN
```

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  Query Match             2.7%;  Score 39.6;  DB 34;  Length 4673;
  Best Local Similarity   60.0%;  Pred. No. 19;
  Matches   66;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy   1379 ataagatttgggggaacctggatgagttttttttttgcatctttaataatttcttatat 1438
          |||  ||||| |  ||  |  |   | | | ||||| |||| ||| | || || | | ||
Db   4033 ATATTATTTGTGTAAAAATTAAGATGATATATTTTTAGCATATTTGACAAATTGTCAAAT 4092

Qy   1439 gttgtagagtatgttttaaaataaatttcaagtatttttttaaaaaactt 1488
             |  | | ||||||  || |||| | |    |||||||| |   ||
Db   4093 TCGTTGTATTCTGTTTTTGAAAAAATATGAGCATTTTTTTTAATATTATT 4142
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```
RESULT  12
AC006803/c
LOCUS       AC006803   299820 bp    DNA             HTG       25-FEB-1999
DEFINITION  Caenorhabditis elegans clone Y53G8A, *** SEQUENCING IN PROGRESS
            ***, 3 unordered pieces.
ACCESSION   AC006803
VERSION     AC006803.2  GI:4309783
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 299820)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Caehorhabditis elegans clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 299820)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Mar 1, 1999 this sequence version replaced gi:4263135.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    76548: contig of 76548 bp in length
            *    76549    76557: gap of unknown length
            *    76558   162292: contig of 85735 bp in length
            *   162293   162300: gap of unknown length
            *   162301   299820: contig of 137520 bp in length.
FEATURES             Location/Qualifiers
     source          1. .299820
                     /organism="Caenorhabditis elegans"
                     /db_xref="taxon:6239"
                     /clone="Y53G8A"
BASE COUNT    98291 a   51999 c   51839 g   96253 t    1438 others
ORIGIN
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  Query Match             2.7%;  Score 39.6;  DB 33;  Length 299820;
  Best Local Similarity   60.0%;  Pred. No. 31;
  Matches   66;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy   1380 taagatttgggggaacctggatgagttttttttttgcatctttaataatttcttatatg 1439
          | | |||| | | || || || |||||||       |   ||    | | ||| ||  |
Db 159048 TGATATTTAGAGTAAACTCGACGAGTTTTGAAAGGTTTTTCAGGCAAATTTTTTTCAAAT 158989

Qy   1440 ttgtagagtatgttttaaaataaatttcaagtatttttttaaaaaacttt 1489
          |   ||  || | ||  || |||||| || || ||||||||||  | |||
Db 158988 ATTCGGAAAATTTGTTTCAAAAAATTTAAAATAATTTTTTAAAACAATTT 158939
```

```
RESULT  13
AC006871/c
LOCUS       AC006871   299820 bp    DNA             HTG       26-FEB-1999
DEFINITION  Caenorhabditis elegans clone Y53G8X, *** SEQUENCING IN PROGRESS
            ***, 3 unordered pieces.
ACCESSION   AC006871
VERSION     AC006871.1  GI:4263477
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
            Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 299820)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Caehorhabditis elegans clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 299820)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    76548: contig of 76548 bp in length
            *    76549    76557: gap of unknown length
            *    76558   162292: contig of 85735 bp in length
            *   162293   162300: gap of unknown length
            *   162301   299820: contig of 137520 bp in length.
FEATURES             Location/Qualifiers
     source          1. .299820
                     /organism="Caenorhabditis elegans"
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                 /db_xref="taxon:6239"
                 /clone="Y53G8X"
BASE COUNT    98291 a  51999 c  51839 g  96253 t   1438 others
ORIGIN


  Query Match             2.7%;  Score 39.6;  DB 33;  Length 299820;
  Best Local Similarity   60.0%;  Pred. No. 31;
  Matches   66;  Conservative    0;  Mismatches   44;  Indels    0;  Gaps    0;

Qy   1380 taagatttgggggaacctggatgagttttttttttgcatctttaataatttcttatatg 1439
          | | |||| | | || || || |||||||       |   ||    | | ||| ||  |
Db 159048 TGATATTTAGAGTAAACTCGACGAGTTTTGAAAGGTTTTTCAGGCAAATTTTTTTCAAAT 158989

Qy   1440 ttgtagagtatgttttaaaataaatttcaagtatttttttaaaaaacttt 1489
            |   ||  || | ||  || |||||| || || ||||||||||| | |||
Db 158988 ATTCGGAAAATTTGTTTCAAAAAATTTAAAATAATTTTTTAAAACAATTT 158939


RESULT  14
DDU73686
LOCUS       DDU73686     1840 bp    DNA             INV       08-DEC-1997
DEFINITION  Dictyostelium discoideum cytosolic glycoprotein FP21 (fpa2) gene,
            complete cds.
ACCESSION   U73686
VERSION     U73686.1  GI:1658023
KEYWORDS    .
SOURCE      Dictyostelium discoideum.
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 1840)
  AUTHORS   West,C.M., Kozarov,E. and Teng-umnuay,P.
  TITLE     The cytosolic glycoprotein FP21 of Dictyostelium discoideum is
            encoded by two genes resulting in a polymorphism at a single amino
            acid position
  JOURNAL   Gene 200 (1-2), 1-10 (1997)
  MEDLINE   98038971
REFERENCE   2  (bases 1 to 1840)
  AUTHORS   West,M.C., Kozarov,E. and Teng-umnuay,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-1996) Anatomy & Cell Biology, University of
            Florida, 1600 SW Archer Rd., Gainesville, FL 32610-0235, USA
FEATURES             Location/Qualifiers
     source          1. .1840
                     /organism="Dictyostelium discoideum"
                     /strain="Ax3"
                     /db_xref="taxon:44689"
     gene            1061. .1703
                     /gene="fpa2"
     CDS             join(1061. .1157,1312. .1703)
                     /gene="fpa2"
                     /note="SKP1-like; similar to the product of the fpal gene"
                     /codon_start=1
                     /product="cytosolic glycoprotein FP21"
                     /protein_id="AAB88390.1"
                     /db_xref="GI:1658024"
                     /translation="MSLVKLESSDEKVFEIEKEIACMSVTIKNMIEDIGESDAPIPLP
                     NVTSTILEKVLDYCRHHHQHPSPQGDDKKDEKRLDDIPPYDRDFCKVDQPTLFELILA
                     ANYLDIKPLLDVTCKTVANMIRGKTPEEIRKIFNIKNDFTPEEEEQIRKENEWCEDKG
                     GN"
     intron          1158. .1311
                     /gene="fpa2"
BASE COUNT      742 a    166 c    170 g    762 t
ORIGIN


  Query Match             2.6%;  Score 39.4;  DB 34;  Length 1840;
  Best Local Similarity   62.9%;  Pred. No. 18;
  Matches   61;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy   1393 aacctggatgagttttttttttgcatctttaataatttcttatatgttgtagagtatgt 1452
           ||| |   |   ||||||||||  || |||  |   || ||  || || |    | | |
Db    870 AACTTTTTTTTTTTTTTTTTTCTATTTTTTTCTATTTTTAATTTTTTTTTTTTT 929

Qy   1453 tttaaaataaatttcaagtatttttttaaaaaacttt 1489
          |||||||  || || |  | |||||  |||||| |||
Db    930 TTTAAAAATAAATTAATTTTTTTTAAAAAAAGTTT 966


RESULT  15
AC004994/c
LOCUS       AC004994     80331 bp    DNA             PRI       21-NOV-1998
DEFINITION  Homo sapiens PAC clone DJ1194E15 from 7p15.3-p21, complete
            sequence.
ACCESSION   AC004994
VERSION     AC004994.1  GI:3900849
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 80331)
  AUTHORS   Drone,K., Ryan,E. and Williamson,A.
  TITLE     The sequence of Homo sapiens PAC clone DJ1194E15
  JOURNAL   Unpublished (1998)
REFERENCE   2  (bases 1 to 80331)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 80331)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-NOV-1998) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Nov 21, 1998 this sequence version replaced gi:3377480.
            SUBMITTED BY:  WUGSC
            Genome Sequencing Center
            Department of Genetics
            Washington University
            St. Louis MO 63108, USA
            http://genome.wustl.edu/gsc
            mailto:sapiens@watson.wustl.edu

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded or sequenced with an alternate
            chemistry; an attempt was made to resolve all sequencing problems,
            such as compressions and repeats; all regions were covered by
            sequence from more than one subclone; and the assembly was
            confirmed by restriction digest.

            MAPPING INFORMATION:
            The sequence of this clone was established as part of a mapping and
            sequencing collaboration between the NHGRI Chromosome 7 Mapping
            Project (Eric D. Green, Director), John D. McPherson in the
            Department of Genetics (Washington University), and the Washington
            University Genome Sequencing Center.  For additional information
            about the map position of this sequence, see
            http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
            mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            This clone was derived from human PAC library RPCI-5, prepared by
            Pieter de Jong and coworkers at the Roswell Park Cancer Institute
            (http://bacpac.med.buffalo.edu) using the method described by
            Ioannou et al., Nature Genetics 6:84-9 (1994).  The library is from
            one male donor.
            The clone may be obtained either from Genome Systems, Inc.
            (http://www.genomesystems.com) or Research Genetics, Inc.
            (http://www.resgen.com); or from Pieter de Jong.
```

```
          VECTOR:  pCYPAC2
          NEIGHBORING SEQUENCE INFORMATION:
          The clone sequenced to the left is GS465N13, 200 bp overlap; the
          clone sequenced to the right is RG264L19, 200 bp overlap.  Actual
          start of this clone is at base position 76644 of GS465N13; actual
          end is at 44319 of RG264L19.
FEATURES             Location/Qualifiers
     source          1. .80331
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /map="7p15.3-p21"
                     /clone_lib="RPCI-5"
                     /clone="DJ1194E15"
     gene            complement(<13. .>79764)
                     /gene="WUGSC:H_DJ1194E15.1"
     CDS             complement(join(<13. .97,18301. .18434,79647. .>79764))
                     /gene="WUGSC:H_DJ1194E15.1"
                     /note="similar to KIAA0600; similar to d1026456
                     (PID:g3043724); H_DJ1194E15.1"
                     /codon_start=1
                     /evidence=not_experimental
                     /protein_id="AAC78618.1"
                     /db_xref="GI:3900850"
                     /translation="TIVKPVAKEFDPDMVLVSAGFDALEGHTPPLGGYKVTAKCFGHL
                     TKQLMTLADGRVVLALEGGHDLTAICDASEACVNALLGNELEPLAEDILHQSPNMNAV
                     ISLQKIIEIQ"
     repeat_region   2455. .2512
                     /rpt_family="AT_rich"
     repeat_region   3372. .3565
                     /rpt_family="L2"
     repeat_region   4099. .4315
                     /rpt_family="L1"
     repeat_region   4316. .4365
                     /rpt_family="(TA)n"
     misc_feature    4483. .5333
                     /gene="WUGSC:H_DJ1194E15.1"
                     /note="nucleolar phosphoprotein B23 pseudogene"
     repeat_region   4958. .5023
                     /rpt_family="(CAT)n"
     repeat_region   5656. .5753
                     /rpt_family="L1"
     repeat_region   5853. .7796
                     /rpt_family="L1"
     repeat_region   7927. .8176
                     /rpt_family="L1"
     repeat_region   8177. .8486
                     /rpt_family="Alu"
     repeat_region   8487. .9690
                     /rpt_family="L1"
     repeat_region   11262. .11310
                     /rpt_family="AT_rich"
     repeat_region   11381. .11577
                     /rpt_family="MER1_type"
     repeat_region   12987. .13102
                     /rpt_family="purine-rich"
     repeat_region   15624. .15929
                     /rpt_family="Alu"
     repeat_region   15989. .16069
                     /rpt_family="Alu"
     repeat_region   16906. .17212
                     /rpt_family="Alu"
     repeat_region   17811. .17894
                     /rpt_family="MIR"
     repeat_region   18501. .18681
                     /rpt_family="MIR"
     repeat_region   18854. .18950
                     /rpt_family="AT_rich"
     repeat_region   19357. .19427
                     /rpt_family="L1"
     repeat_region   19473. .19619
                     /rpt_family="L1"
     repeat_region   19631. .19916
                     /rpt_family="L1"
     repeat_region   20235. .20524
                     /rpt_family="L1"
     repeat_region   20590. .20621
                     /rpt_family="AT_rich"
     repeat_region   20683. .20891
                     /rpt_family="MaLR"
     repeat_region   20896. .21144
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     repeat_region   21364. .21482
                     /rpt_family="purine-rich"
     repeat_region   22050. .22083
                     /rpt_family="AT_rich"
     repeat_region   22088. .22447
                     /rpt_family="L1"
     repeat_region   23613. .23634
                     /rpt_family="AT_rich"
     repeat_region   23754. .23794
                     /rpt_family="(CA)n"
     repeat_region   24294. .24587
                     /rpt_family="Alu"
     repeat_region   24901. .24939
                     /rpt_family="AT_rich"
     repeat_region   25243. .25281
                     /rpt_family="AT_rich"
     repeat_region   25327. .25356
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     repeat_region   25395. .25457
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     repeat_region   27576. .27622
                     /rpt_family="(TGGA)n"
     repeat_region   27713. .27849
                     /rpt_family="MIR"
     repeat_region   27850. .27880
                     /rpt_family="L2"
     repeat_region   27889. .28176
                     /rpt_family="Alu"
     repeat_region   28711. .28846
                     /rpt_family="L2"
     repeat_region   28829. .28909
                     /rpt_family="MIR"
     repeat_region   31608. .31713
                     /rpt_family="MER1_type"
     repeat_region   31897. .31947
                     /rpt_family="AT_rich"
     repeat_region   32013. .33329
                     /rpt_family="L1"
     repeat_region   33329. .34415
                     /rpt_family="L1"
     repeat_region   35816. .35997
                     /rpt_family="L2"
     repeat_region   36396. .36522
                     /rpt_family="MIR"
     repeat_region   37800. .37879
                     /rpt_family="MIR"
     repeat_region   38441. .38463
                     /rpt_family="(CAA)n"
     repeat_region   39574. .39889
                     /rpt_family="MER1_type"
     repeat_region   39911. .40294
                     /rpt_family="MaLR"
     repeat_region   41534. .41740

  Query Match             2.6%;  Score 39.4;  DB 40;  Length 80331;
  Best Local Similarity   56.6%;  Pred. No. 29;
  Matches   73;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy   1357 agatcagaaactctgttcccagcataagatttgggggaacctggatgagtttttttttttg 1416
            | |||| |  |||  |||      |  | || || |||  || |||||   |||| | |
Db  77646 AAATCAAAGTTCTTATCCTGAATCAGTAGTTAGGTGAAATTGCATGAGGCATTTTCTGTA 77587

Qy   1417 catctttaataatttcttatatgttgtagagtatgttttaaaataaatttcaagtatttt 1476
             | ||  || |      | |||||  | |  |||  | | |||| ||||    | ||||
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Db  77586 TTTTTTCCATTAAAAAGAAAATGTTTCATAAAATGGATGAGAATAGATTTTTTTTTTTTT 77527

Qy   1477 tttaaaaaa 1485
          ||||| | |
Db  77526 TTTAAGACA 77518
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Search completed: April 23, 2000, 02:20:29
Job time: 3094 sec

****

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 18 14:00:52 2000; MasPar time 93.97 Seconds
312.120 Million cell updates/sec

Tabular output not generated.

Title: >US-09-490-187-2
Description: (1-423) from US09490187.pep
Perfect Score: 3111
Sequence: 1 MALKVLLEQEKTFFTLLVLL.....AVIHPATQTSLQVRQRLGSL 423

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.756; Variance 76.185; scale 0.614

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	205	6.6	186	14	O72735	A53R PROTEIN.	8.55e-21
2	201	6.5	186	14	Q9WJB4	TUMOUR NECROSIS FACTOR	5.80e-20
3	187	6.0	186	14	Q9YP87	SOLUBLE TNF RECEPTOR C	4.32e-17
4	161	5.2	283	6	Q9XSZ8	HVEAS.	6.13e-12
5	152	4.9	348	14	O57108	TUMOR NECROSIS FACTOR	3.19e-10
6	152	4.9	348	14	O57103	TUMOR NECROSIS FACTOR	3.19e-10
7	152	4.9	348	14	O57277	TUMOR NECROSIS FACTOR	3.19e-10
8	152	4.9	349	14	O57102	TUMOR NECROSIS FACTOR	3.19e-10
9	152	4.9	349	14	O57101	TUMOR NECROSIS FACTOR	3.19e-10
10	152	4.9	349	14	O57100	TUMOR NECROSIS FACTOR	3.19e-10
11	152	4.9	349	14	O57291	TUMOR NECROSIS FACTOR	3.19e-10
12	152	4.9	349	14	O57099	TUMOR NECROSIS FACTOR	3.19e-10
13	150	4.8	253	4	O00276	LYMPHOCYTE ASSOCIATED	7.58e-10
14	150	4.8	277	4	O14866	SOLUBLE DEATH RECEPTOR	7.58e-10
15	150	4.8	350	14	O57116	TUMOR NECROSIS FACTOR	7.58e-10
16	149	4.8	350	14	O57123	TUMOR NECROSIS FACTOR	1.17e-09
17	148	4.8	355	14	Q85308	SECRETED RECEPTOR BIND	1.79e-09
18	150	4.8	372	4	O00279	LYMPHOCYTE ASSOCIATED	7.58e-10
19	150	4.8	380	4	O00280	LYMPHOCYTE ASSOCIATED	7.58e-10
20	150	4.8	418	4	O00275	LYMPHOCYTE ASSOCIATED	7.58e-10
21	150	4.8	426	4	O14865	DEATH RECEPTOR 3 BETA.	7.58e-10
22	143	4.6	326	14	O57120	TUMOR NECROSIS FACTOR	1.51e-08
23	144	4.6	351	14	O73559	H4R PROTEIN.	9.90e-09
24	141	4.5	326	14	O57122	TUMOR NECROSIS FACTOR	3.52e-08
25	140	4.5	347	14	O57115	TUMOR NECROSIS FACTOR	5.35e-08
26	141	4.5	349	14	O57305	TUMOR NECROSIS FACTOR	3.52e-08
27	141	4.5	351	14	O57117	TUMOR NECROSIS FACTOR	3.52e-08
28	141	4.5	368	13	O57408	SUBGROUP E ALV RECEPTO	3.52e-08
29	137	4.4	267	6	O02764	OX40 PRECURSOR (FRAGME	1.87e-07
30	138	4.4	322	14	O72761	K2R PROTEIN.	1.23e-07
31	137	4.4	347	14	O57119	TUMOR NECROSIS FACTOR	1.87e-07
32	137	4.4	351	14	O57121	TUMOR NECROSIS FACTOR	1.87e-07
33	137	4.4	360	14	O57118	TUMOR NECROSIS FACTOR	1.87e-07
34	133	4.3	314	4	Q14293	FAS SOLUBLE PROTEIN.	9.72e-07
35	130	4.2	349	14	O57284	TUMOR NECROSIS FACTOR	3.29e-06
36	130	4.2	349	14	O57098	TUMOR NECROSIS FACTOR	3.29e-06
37	128	4.1	283	4	Q92956	HERPESVIRUS ENTRY MEDI	7.37e-06
38	128	4.1	320	14	O57079	TUMOR NECROSIS FACTOR	7.37e-06
39	128	4.1	348	14	Q85407	HOMOLOG OF VACCINIA VI	7.37e-06
40	128	4.1	348	14	O57112	TUMOR NECROSIS FACTOR	7.37e-06
41	128	4.1	349	14	O57110	TUMOR NECROSIS FACTOR	7.37e-06
42	128	4.1	349	14	Q89118	SOMALIA-1977 RIGHT NEA	7.37e-06
43	128	4.1	349	14	O57111	TUMOR NECROSIS FACTOR	7.37e-06
44	128	4.1	349	14	Q89098	GARCIA-1966 RIGHT NEAR	7.37e-06
45	128	4.1	471	6	O19131	TUMOR NECROSIS FACTOR-	7.37e-06

ALIGNMENTS

RESULT 1
ID O72735 PRELIMINARY; PRT; 186 AA.
AC O72735;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE A53R PROTEIN.
GN A53R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RX MEDLINE; 98229462.
RA SHCHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A.,
RA RYAZANKINA O.I., GUTOROV V.V., KOTWAL G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins.";
RL Virology 243:432-460(1998).
DR EMBL; Y15035; CAA75273.1; -.
DR HSSP; P25942; 1CDF.
DR PFAM; PF00020; TNFR_c6; 2.
SQ SEQUENCE 186 AA; 20482 MW; C635B516 CRC32;

Query Match 6.6%; Score 205; DB 14; Length 186;
Best Local Similarity 33.3%; Pred. No. 8.55e-21;
Matches 37; Conservative 23; Mismatches 40; Indels 11; Gaps 10;

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Db      34 NGSCDEGEYLDKRHNQC--CNQCPPG-EFAKVRCS-G-SDNTKCERCPPHTYTAIPNYSN 88
           :| | : |: | |   |  |||| || |::|  |: | :::: |  |  | :    : :
Qy      31 SGDCRQQEFRD-RSGNCVPCNQCGPGMELSKE-CGFGYGEDAQCVACRLHRFKEDWGFQK 88

Db      89 GCHQCRKCPW-GSFDKVKCTGTQNSKCS-CLPGWYCATDSSQTEDCRDCVP 137
             |  |  |:    |:| :|::| :: |: |||| |  |     :|  :|||
Qy      89 -CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQD-MECVP 137
```

RESULT 2
ID Q9WJB4 PRELIMINARY; PRT; 186 AA.
AC Q9WJB4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

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DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOUR NECROSIS FACTOR RECEPTOR PRECURSOR.
GN   A53R.
OS   Vaccinia virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LISTER;
RX   MEDLINE; 99226947.
RA   ALCAMI A., KHANNA A., PAUL N., SMITH J.L.;
RT   "Vaccinia virus strains Lister, USSR and Evans express soluble and
RT   cell-surface tumour necrosis factor receptors.";
RL   J. Gen. Virol. 80:949-959(1999).
DR   EMBL; Y17728; CAB41042.1; -.
KW   Signal; Receptor.
FT   SIGNAL       1      22       POTENTIAL.
SQ   SEQUENCE   186 AA;  20646 MW;  6D548A28 CRC32;

  Query Match             6.5%;  Score 201;  DB 14;  Length 186;
  Best Local Similarity  32.4%;  Pred. No. 5.80e-20;
  Matches    36;  Conservative   22;  Mismatches  42;  Indels  11;  Gaps  10;

Db      34 NGACDEGEYLDKRHNQC--CNQCPPG-EFAKVRCN-G-NDNTKCERCPPHTYTAIPNYSN 88
           :| | : |: | |    |  |||| || |::|  |  |  ::: |  |  | :     : :
Qy      31 SGDCRQQEFRD-RSGNCVPCNQCGPGMELSKE-CGFGYGEDAQCVACRLHRFKEDWGFQK 88

Db      89 GCHQCRKCPT-GSFDKVKCTGTQNSKCS-CLPGWYCATDSSQTEDCRDCIP 137
             | |  |:    |:| :|::| :: |: |||| |  |     :|  :|:|
Qy      89 -CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQD-MECVP 137


RESULT    3
ID   Q9YP87      PRELIMINARY;      PRT;   186 AA.
AC   Q9YP87;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   SOLUBLE TNF RECEPTOR CRMC.
GN   CRMC.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BRIGHTON REDGENE;
RA   SMITH C.A., GOODWIN R.G., PICKUP D.J.;
RT   "Cowpox virus Encodes a second soluble TNF receptor (CrmC) Distinct
RT   from CrmB.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U55052; AAD10325.1; -.
KW   Receptor.
SQ   SEQUENCE   186 AA;  20372 MW;  2A90DC98 CRC32;

  Query Match             6.0%;  Score 187;  DB 14;  Length 186;
  Best Local Similarity  30.0%;  Pred. No. 4.32e-17;
  Matches    33;  Conservative   28;  Mismatches  40;  Indels   9;  Gaps   9;

Db      34 NGSCDDGEYLDKTHN-QCCNRCPPG-EFAKIRCS-G-SDNTKCERCPPHTYTTVPNYSNG 89
           :| | : |: |:: |   ||:| || |::|  |: | :::: |  |  | :     : :
Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKE-CGFGYGEDAQCVACRLHRFKEDWGFQK- 88

Db      90 CHQCRKCPT-GSFDKVKCTGTQNSKCS-CLPGWFCATDSSKTEDCRDCIP 137
           |  |  |:    |:| :|::| :: |: |||| :  |     :|  :|:|
Qy      89 CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKTKLVGFQD-MECVP 137


RESULT    4
ID   Q9XSZ8      PRELIMINARY;      PRT;   283 AA.
AC   Q9XSZ8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   HVEAS.
GN   HVEAS.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
OC   Chlorocebus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 99296730.
RA   FOSTER T.P., CHOULJENKO V.N., KOUSOULAS K.G.;
RT   "Functional characterization of the HveA homolog specified by African
RT   green monkey kidney cells with a herpes simplex virus expressing the
RT   green fluorescence protein.";
RL   Virology 258:365-374(1999).
DR   EMBL; AF147720; AAD37381.1; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
SQ   SEQUENCE   283 AA;  30199 MW;  9B499EAB CRC32;

  Query Match             5.2%;  Score 161;  DB 6;  Length 283;
  Best Local Similarity  27.4%;  Pred. No. 6.13e-12;
  Matches    31;  Conservative   27;  Mismatches  46;  Indels   9;  Gaps   8;

Db      20 ILTLVLYLTFLGSSCYAPALPSCKEDEYPV-GSEC--CPKCGPGFHVRQACG-E-QTGTV 74
           ::||:: | :|:    :     |:::|:   :::|  |  ||||  :   ||     :
Qy      13 FFTLLVLLGYLSCKV-TCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQ 71

Db      75 CEPCSPGTYIAHFNGLSKCLQCQMCDPAMGLRTSRNCSTTANALCG-CSPGHF 126
           | :|    :     |: ||  |  |     :: : |||:|::|:|| | || :
Qy      72 CVACRLHRFKEDW-GFQKCKPCLDCAVVNRFQKA-NCSATSDAICGDCLPGFY 122


RESULT    5
ID   O57108      PRELIMINARY;      PRT;   348 AA.
AC   O57108;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1970 (CONGO-8);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88142; AAB94367.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  28F1C77C CRC32;

  Query Match             4.9%;  Score 152;  DB 14;  Length 348;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db      29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: | :   ::|| :|    |      :| |
Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db      84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
           :|   |   |: :  :|::| : || :| ||:|
Qy      90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT    6
ID   O57103      PRELIMINARY;      PRT;   348 AA.
AC   O57103;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
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DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1979 (79-0005);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87847; AAB94364.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   348 AA;  38184 MW;  EF87B2D2 CRC32;

  Query Match           4.9%;  Score 152;  DB 14;  Length 348;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db     29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db     84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
           :|   |   |: :  :|::| : || :| ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT    7
ID   O57277      PRELIMINARY;      PRT;   348 AA.
AC   O57277;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1996(96-17), ZAIRE-1996 (96-16);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88543; AAB94378.1; -.
DR   EMBL; U87841; AAB94358.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   348 AA;  38212 MW;  1AAABB69 CRC32;

  Query Match           4.9%;  Score 152;  DB 14;  Length 348;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db     29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db     84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
           :|   |   |: :  :|::| : || :| ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT    8
ID   O57102      PRELIMINARY;      PRT;   349 AA.
AC   O57102;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BENIN-1978 (78-3945);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87846; AAB94363.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   349 AA;  38308 MW;  17182545 CRC32;

  Query Match           4.9%;  Score 152;  DB 14;  Length 349;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db     29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db     84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
           :|   |   |: :  :|::| : || :| ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT    9
ID   O57101      PRELIMINARY;      PRT;   349 AA.
AC   O57101;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ZAIRE-1977 (77-0666);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87845; AAB94362.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   349 AA;  38311 MW;  4F4F8AF1 CRC32;

  Query Match           4.9%;  Score 152;  DB 14;  Length 349;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db     29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db     84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
           :|   |   |: :  :|::| : || :| ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   10
ID   O57100      PRELIMINARY;      PRT;   349 AA.
AC   O57100;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NIGERIA-1971 (71-0082);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87844; AAB94361.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   349 AA;  38239 MW;  F8871DD2 CRC32;

  Query Match             4.9%;  Score 152;  DB 14;  Length 349;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db      29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db      84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
             :|   |   |: :  :|::| : || :| ||:|
Qy      90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   11
ID   O57291      PRELIMINARY;      PRT;   349 AA.
AC   O57291;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VARIOUS STRAINS;
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U88144; AAB94369.1; -.
DR   EMBL; U87842; AAB94359.1; -.
DR   EMBL; U87994; AAB94365.1; -.
DR   EMBL; U87995; AAB94366.1; -.
DR   EMBL; U88143; AAB94368.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   349 AA;  38295 MW;  7313FCF9 CRC32;

  Query Match             4.9%;  Score 152;  DB 14;  Length 349;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db      29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db      84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
             :|   |   |: :  :|::| : || :| ||:|
Qy      90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   12
ID   O57099      PRELIMINARY;      PRT;   349 AA.
AC   O57099;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SIERRA LEONE-1970 (70-0266);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U87843; AAB94360.1; -.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   349 AA;  38321 MW;  5315315C CRC32;

  Query Match             4.9%;  Score 152;  DB 14;  Length 349;
  Best Local Similarity  30.9%;  Pred. No. 3.19e-10;
  Matches    29;  Conservative   20;  Mismatches  36;  Indels   9;  Gaps   8;

Db      29 NGKCKDNEYRSRN-LC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSDTFTSHNNHLQAC 83
           :| |:: |:| |:  |  |  | ||   |: |  :   ::|| :|    |      :| |
Qy      31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKC 89

Db      84 LSCNGRCDS-NQVETRSCNTTHNRIC-ECSPGYY 115
             :|   |   |: :  :|::| : || :| ||:|
Qy      90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   13
ID   O00276      PRELIMINARY;      PRT;   253 AA.
AC   O00276;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 97272273.
RA   SCREATON G.R., XU X.N., OLSEN A.L., COWPER A.E., TAN R.,
RA   MCMICHAEL A.J., BELL J.I.;
RT   "LARD: a new lymphoid-specific death domain containing receptor
RT   regulated by alternative pre-mRNA splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR   EMBL; U94503; AAC51308.1; -.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   253 AA;  26934 MW;  A21C863E CRC32;

  Query Match             4.8%;  Score 150;  DB 4;  Length 253;
  Best Local Similarity  52.9%;  Pred. No. 7.58e-10;
  Matches    18;  Conservative    5;  Mismatches  10;  Indels   1;  Gaps   1;

Db     138 CQPCLDCGALHRHTRLLCS-RRDTDCGTCLPGFY 170
           | |||||: ::|  :  ||   |: || ||||||
Qy      89 CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   14
ID   O14866      PRELIMINARY;      PRT;   277 AA.
AC   O14866;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   SOLUBLE DEATH RECEPTOR 3 BETA.
GN   DR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WARZOCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,
```

```
RA   SALLES G.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026071; AAB82288.1; -.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   277 AA;  29111 MW;  06E165C7 CRC32;

  Query Match             4.8%;  Score 150;  DB 4;  Length 277;
  Best Local Similarity  52.9%;  Pred. No. 7.58e-10;
  Matches    18;  Conservative    5;  Mismatches  10;  Indels   1;  Gaps   1;

Db    138 CQPCLDCGALHRHTRLLCS-RRDTDCGTCLPGFY 170
          | ||||| : ::|  :  ||   |: || ||||||
Qy     89 CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   15
ID   O57116      PRELIMINARY;      PRT;   350 AA.
AC   O57116;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN   CRMB.
OS   Cowpox virus (CPV).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MUNICH OPV 89/2(CAT);
RA   LOPAREV V.N., PARSONS J.M., ESPOSITO J.J.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U90226; AAB94382.1; -.
DR   HSSP; P25942; 1CDF.
DR   PFAM; PF00020; TNFR_c6; 2.
SQ   SEQUENCE   350 AA;  38216 MW;  5FF88E39 CRC32;

  Query Match             4.8%;  Score 150;  DB 14;  Length 350;
  Best Local Similarity  29.8%;  Pred. No. 7.58e-10;
  Matches    28;  Conservative   19;  Mismatches  40;  Indels   7;  Gaps   6;

Db     29 NGKCKDNEY-NRHNLC--CLSCPPGTYASRLCDSKTNTNTQCTPCGSDTFTSRNNHLPAC 85
          :| |:: |: :|   |  |  | ||   |: |      ::|| :|    |   :  :  |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKC 89

Db     86 LSCNGRCDS-NQVETRSCNTTHNRIC-DCAPGYY 117
           :|   |   |: :  :|::| : || || ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


Search completed: Tue Apr 18 14:02:30 2000
Job time : 98 secs.
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MPSRCH (TM)

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MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:          Tue Apr 18 13:59:51 2000;  MasPar time 39.25 Seconds
                                            321.889 Million cell updates/sec
Tabular output not generated.

Title:           >US-09-490-187-2
Description:     (1-423) from US09490187.pep
Perfect Score:   3111
Sequence:        1 MALKVLLEQEKTFFTLLVLL..........AVIHPATQTSLQVRQRLGSL 423

Scoring table:   PAM 150
                 Gap 11

Searched:        82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        swiss-prot38
                   1:swissprot

Statistics:      Mean 48.063;  Variance 74.860;  scale 0.642
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	170	5.5	272	1	OX40_MOUSE	OX40L RECEPTOR PRECURS	1.94e-14
2	149	4.8	271	1	OX40_RAT	OX40L RECEPTOR PRECURS	2.86e-10
3	150	4.8	417	1	WSL1_HUMAN	WSL-1 PROTEIN PRECURSO	1.83e-10
4	146	4.7	416	1	NGFR_CHICK	LOW-AFFINITY NERVE GRO	1.08e-09
5	146	4.7	461	1	TNR1_PIG	TUMOR NECROSIS FACTOR	1.08e-09
6	142	4.6	454	1	TNR1_MOUSE	TUMOR NECROSIS FACTOR	6.22e-09
7	143	4.6	455	1	TNR1_HUMAN	TUMOR NECROSIS FACTOR	4.02e-09
8	136	4.4	435	1	TNRC_HUMAN	LYMPHOTOXIN-BETA RECEP	8.24e-08
9	133	4.3	335	1	FASA_HUMAN	FASL RECEPTOR PRECURSO	2.94e-07
10	130	4.2	326	1	VT2_MYXVL	TUMOR NECROSIS FACTOR	1.03e-06
11	130	4.2	415	1	TNRC_MOUSE	LYMPHOTOXIN-BETA RECEP	1.03e-06
12	130	4.2	461	1	TNR1_RAT	TUMOR NECROSIS FACTOR	1.03e-06
13	127	4.1	327	1	FASA_MOUSE	FASL RECEPTOR PRECURSO	3.58e-06
14	128	4.1	349	1	VC22_VARV	PROTEIN C22/B28 HOMOLO	2.37e-06
15	126	4.1	1192	1	LMG2_MOUSE	LAMININ GAMMA-2 CHAIN	5.39e-06
16	125	4.0	255	1	41BB_HUMAN	4-1BB LIGAND RECEPTOR	8.11e-06
17	125	4.0	474	1	TNR2_MOUSE	TUMOR NECROSIS FACTOR	8.11e-06
18	122	3.9	324	1	FASA_RAT	FASL RECEPTOR PRECURSO	2.73e-05
19	120	3.9	332	1	FASA_PIG	FASL RECEPTOR PRECURSO	6.08e-05
20	122	3.9	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	2.73e-05
21	121	3.9	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	4.08e-05
22	120	3.9	461	1	TNR2_HUMAN	TUMOR NECROSIS FACTOR	6.08e-05
23	119	3.8	323	1	FASA_BOVIN	FASL RECEPTOR PRECURSO	9.05e-05
24	118	3.8	1193	1	LMG2_HUMAN	LAMININ GAMMA-2 CHAIN	1.34e-04
25	115	3.7	1680	1	FUR2_DROME	FURIN-LIKE PROTEASE 2	4.34e-04
26	111	3.6	277	1	CD40_HUMAN	CD40L RECEPTOR PRECURS	2.01e-03
27	110	3.5	3075	1	LMA1_HUMAN	LAMININ ALPHA-1 CHAIN	2.94e-03
28	108	3.5	3084	1	LMA1_MOUSE	LAMININ ALPHA-1 CHAIN	6.21e-03
29	107	3.4	250	1	CD27_MOUSE	CD27L RECEPTOR PRECURS	9.00e-03
30	105	3.4	256	1	41BB_MOUSE	4-1BB LIGAND RECEPTOR	1.88e-02
31	105	3.4	260	1	CD27_HUMAN	CD27L RECEPTOR PRECURS	1.88e-02
32	106	3.4	277	1	OX40_HUMAN	OX40L RECEPTOR PRECURS	1.30e-02
33	106	3.4	703	1	SAT1_RAT	SULFATE ANION TRANSPOR	1.30e-02
34	106	3.4	2871	1	FBN1_MOUSE	FIBRILLIN 1 PRECURSOR.	1.30e-02
35	104	3.3	289	1	CD40_MOUSE	CD40L RECEPTOR PRECURS	2.70e-02
36	104	3.3	956	1	TSP3_MOUSE	THROMBOSPONDIN 3 PRECU	2.70e-02
37	103	3.3	2871	1	FBN1_BOVIN	FIBRILLIN 1 PRECURSOR	3.87e-02
38	103	3.3	3635	1	LMA5_MOUSE	LAMININ ALPHA-5 CHAIN	3.87e-02
39	99	3.2	103	1	VA53_VACCC	PROTEIN A53.	1.59e-01
40	99	3.2	103	1	VA53_VACCV	PROTEIN A53.	1.59e-01
41	99	3.2	215	1	OS25_PLAGA	25 KD OOKINETE SURFACE	1.59e-01
42	98	3.2	400	1	LMB_HIRME	LAMININ B-CHAIN (FRAGM	2.26e-01
43	99	3.2	1184	1	FBL2_HUMAN	FIBULIN-2 PRECURSOR.	1.59e-01
44	101	3.2	1607	1	LMG1_MOUSE	LAMININ GAMMA-1 CHAIN	7.90e-02
45	99	3.2	3106	1	LMA2_MOUSE	LAMININ ALPHA-2 CHAIN	1.59e-01

ALIGNMENTS

```
RESULT    1
ID   OX40_MOUSE     STANDARD;      PRT;   272 AA.
AC   P47741;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN   TXGP1 OR OX40.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE; 94044750.
RA   CALDERHEAD D.M., BUHLMANN J.E., VAN DEN EERTWEGH A.J.,
RA   CLAASSEN E., NOELLE R.J., FELL H.;
RT   "Cloning of mouse Ox40: a T cell activation marker that may mediate
RT   T-B cell interactions.";
RL   J. Immunol. 151:5261-5271(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95255413.
RA   BIRKELAND M.L., COPELAND N.G., GILBERT D.J., JENKINS N.A.,
RA   BARCLAY A.N.;
RT   "Gene structure and chromosomal localization of the mouse homologue
RT   of rat OX40 protein.";
RL   Eur. J. Immunol. 25:926-930(1995).
CC   -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z21674; CAA79772.1; -.
DR   EMBL; X85214; CAA59476.1; -.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:104512; TXGP1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PFAM; PF00020; TNFR_c6; 3.
```

```
KW   Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    272       OX40L RECEPTOR.
FT   DOMAIN       20    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    236       POTENTIAL.
FT   DOMAIN      237    272       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       26    165       4 X TNFR-CYS.
FT   REPEAT       26     61       TNFR-CYS 1.
FT   REPEAT       62    103       TNFR-CYS 2.
FT   REPEAT      104    124       TNFR-CYS 3 (INCOMPLETE).
FT   REPEAT      125    165       TNFR-CYS 4.
FT   CARBOHYD    144    144       POTENTIAL.
FT   CONFLICT     15     15       A -> G (IN REF. 2).
SQ   SEQUENCE   272 AA;  30153 MW;  67D1B978 CRC32;

  Query Match           5.5%;  Score 170;  DB 1;  Length 272;
  Best Local Similarity  27.3%;  Pred. No. 1.94e-14;
  Matches    48;  Conservative   36;  Mismatches  78;  Indels  14;  Gaps  11;

Db       9 TALLLLA-LTLGVTARRLNCVKHTYPS-GHKC--CRECQPGHGMVSRCD--HTRDTLCHP 62
           | |:||: |:  ||    :|  : :   : :|  | :| ||  :   |      |: | :
Qy      15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db      63 CETGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVC-RCRPGTQPRQD-SGYKLG 120
           |    ::|   :: || | :|   :  : | ||::| |::|  | ||   :    |:
Qy      75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQ-D 132

Db     121 VDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAV-CED-RSLLATLL 174
           ::|||  |  :|  :  | :  |   :  :  |   :| || |   ::| :||
Qy     133 MECVPC--GDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALATVLLALL 186


RESULT    2
ID   OX40_RAT       STANDARD;      PRT;   271 AA.
AC   P15725;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN   TXGP1L OR OX40.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=T-CELL;
RX   MEDLINE; 90214614.
RA   MALLETT S., FOSSUM S., BARCLAY A.N.;
RT   "Characterization of the MRC OX40 antigen of activated CD4 positive T
RT   lymphocytes -- a molecule related to nerve growth factor receptor.";
RL   EMBO J. 9:1063-1068(1990).
CC   -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X17037; CAA34897.1; -.
DR   PIR; S08036; S08036.
DR   PIR; S12783; S12783.
DR   HSSP; P25942; 1CDF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PFAM; PF00020; TNFR_c6; 3.
KW   Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    271       OX40L RECEPTOR.
FT   DOMAIN       20    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    235       POTENTIAL.
FT   DOMAIN      236    271       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       25    164       4 X TNFR-CYS.
FT   REPEAT       25     60       TNFR-CYS 1.
FT   REPEAT       61    102       TNFR-CYS 2.
FT   REPEAT      103    123       TNFR-CYS 3 (INCOMPLETE).
FT   REPEAT      124    164       TNFR-CYS 4.
FT   CARBOHYD    143    143       POTENTIAL.
SQ   SEQUENCE   271 AA;  29895 MW;  65460ED2 CRC32;

  Query Match           4.8%;  Score 149;  DB 1;  Length 271;
  Best Local Similarity  29.1%;  Pred. No. 2.86e-10;
  Matches    39;  Conservative   27;  Mismatches  57;  Indels  11;  Gaps   8;

Db       9 TAFLLLG-LSLGVTVKL-NCVKDTYPS-GHKC--CRECQPGHGMVSRCD--HTRDTVCHP 61
           | ::||| ||  ||    :|  : :   : :|  | :| ||  :   |      |: | :
Qy      15 TLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVA 74

Db      62 CEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVC-QCRPGTQPRQDSSHKLGV 120
           |    ::|   :: || | :|   :  : | ||::| |::| :| ||   :        :
Qy      75 CRLHRFKEDWGFQKCKPCLDCAVVNRFQ-KANCSATSDAICGDCLPGFYRKTKLVGFQDM 133

Db     121 DCVPC--PPGHFSP 132
           :||||  ||  : |
Qy     134 ECVPCGDPPPPYEP 147


RESULT    3
ID   WSL1_HUMAN     STANDARD;      PRT;   417 AA.
AC   Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-DEC-1999 (Rel. 39, Last annotation update)
DE   WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-
DE   MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)
DE   (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED
DE   RECEPTOR OF DEATH) (LARD).
GN   TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.
RC   TISSUE=LYMPHOID;
RX   MEDLINE; 97088617.
RA   KITSON J., RAVEN T., JIANG Y.-P., GOEDDEL D.V., GILES K.M., PUN K.-T.,
RA   GRINHAM C.J., BROWN R., FARROW S.N.;
RT   "A death-domain-containing receptor that mediates apoptosis.";
RL   Nature 384:372-375(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;
RX   MEDLINE; 97081063.
RA   CHINNAIYAN A.M., O'ROURKE K., YU G.-L., LYONS R.H., GARG M.,
RA   DUAN D.R., XING L., GENTZ R., NI J., DIXIT V.M.;
RT   "Signal transduction by DR3, a death domain-containing receptor
RT   related to TNFR-1 and CD95.";
RL   Science 274:990-992(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   DEGLI-ESPOSTI M.A., DIN W.S., COSMAN D., SMITH C.A., GOODWIN R.G.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=HEART;
RA   MARSTERS S.A., SHERIDAN J.P., DONAHUE C.J., PITTI R.M., GRAY C.L.,
RA   GODDARD A.D., BAUER K.D., ASHKENAZI A.;
RT   "Apo-3, a new member of the tumor necrosis factor receptor family,
RT   contains a death domain and activates apoptosis and NF-kappa-B.";
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RL   Curr. Biol. 6:1669-1676(1996).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   SCREATON G.R., XU X.-N., OLSEN A.L., COWPER A.E., TAN R.,
RA   MCMICHAEL A.J., BELL J.I.;
RT   "LARD: a new lymphoid-specific death domain containing receptor
RT   regulated by alternative pre-mRNA splicing.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN   [6]
RP   SEQUENCE OF 4-417 FROM N.A.
RC   TISSUE=BRAIN, AND FETAL LUNG;
RX   MEDLINE; 97205335.
RA   BODMER J.-L., BURNS K., SCHNEIDER P., HOFMANN K., STEINER V.,
RA   THOME M., BORNAND T., HAHNE M., SCHROETER M., WILSON A., FRENCH L.E.,
RA   BROWNING J.L., MACDONALD H.R., TSCHOPP J.;
RT   "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT   to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL   Immunity 6:79-88(1997).
RN   [7]
RP   SEQUENCE OF 7-417 FROM N.A.
RC   TISSUE=BRAIN;
RA   CHAUDHARY P.M., HOOD L.E.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
CC       (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE. MAY
CC       PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.
CC   -!- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
CC       THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNRF1 RECEPTOR TO
CC       ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS: THREE ISOFORMS; WSL-1/LARD-1A (SHOWN HERE),
CC       WSL-S1/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC       LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC       COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC   -!- PTM: GLYCOSYLATED (PROBABLE).
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y09392; CAA70561.1; -.
DR   EMBL; Y09392; CAA70559.1; -.
DR   EMBL; Y09392; CAA70560.1; -.
DR   EMBL; U72763; AAC50819.1; -.
DR   EMBL; U83599; AAB41434.1; -.
DR   EMBL; U83600; AAB41435.1; -.
DR   EMBL; U78029; AAB40918.1; -.
DR   EMBL; U74611; AAB39714.1; -.
DR   EMBL; U94501; AAC51306.1; -.
DR   EMBL; U94504; AAC51309.1; -.
DR   EMBL; U75380; AAC51192.1; -.
DR   EMBL; U75381; AAC51193.1; -.
DR   EMBL; U83597; AAB41432.1; -.
DR   HSSP; P19438; 1TNR.
DR   MIM; 603366; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 2.
DR   PFAM; PF00531; death; 1.
KW   Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
KW   Repeat.
FT   SIGNAL       1     24       POTENTIAL.
FT   CHAIN       25    417       WSL-1 PROTEIN.
FT   DOMAIN      25    199       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   200    220       POTENTIAL.
FT   DOMAIN      223   417       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       34   192       4 X TNFR-CYS.
FT   REPEAT       34    71       TNFR-CYS 1.
FT   REPEAT       72   115       TNFR-CYS 2.
FT   REPEAT      116   163       TNFR-CYS 3.
FT   REPEAT      164   192       TNFR-CYS 4.
FT   DOMAIN      332   413       DEATH DOMAIN.
FT   CARBOHYD     67    67       POTENTIAL.
FT   CARBOHYD    106   106       POTENTIAL.
FT   VARSPLIC    182   218       STLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGA ->
FT                               VLGPGAPGWPCGPPPAWGHPDLHIPPLLASQAPGYCR (IN
FT                               ISOFORM WSL-S1).
FT   VARSPLIC    219   417       MISSING (IN ISOFORM WSL-S1).
FT   VARSPLIC    200   253       MFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
FT                               MEALTPPPATHLS -> SRWCAGNARGRTGMDRGEAGEEGG
FT                               NHPTPTSCFQCSGSRCSWLALWSPSCLGPP (IN
FT                               ISOFORM WSL-S2).
FT   VARSPLIC    254   417       MISSING (IN ISOFORM WSL-S2).
FT   MUTAGEN     354   354       L->A: SUPPRESSES HOMODIMERIZATION, TNFR1
FT                               INTERACTION, AND APOPTOSIS INDUCTION.
FT   MUTAGEN     356   356       L->A: SUPPRESSES HOMODIMERIZATION, AND
FT                               TNFR1 INTERACTION.
FT   MUTAGEN     373   373       D->A: SUPPRESSES HOMODIMERIZATION, AND
FT                               TNFR1 INTERACTION.
FT   CONFLICT      4     6       RPR -> AAA (IN REF. 6).
FT   CONFLICT     60    60       P -> H (IN REF. 7).
FT   CONFLICT    167   167       P -> L (IN REF. 6 AND 7).
FT   CONFLICT    312   312       A -> R (IN REF. 1).
FT   CONFLICT    370   370       R -> L (IN REF. 1).
FT   CONFLICT    381   381       R -> H (IN REF. 1).
SQ   SEQUENCE   417 AA;  45385 MW;  3AEEF0A5 CRC32;

  Query Match           4.8%;  Score 150;  DB 1;  Length 417;
  Best Local Similarity  52.9%;  Pred. No. 1.83e-10;
  Matches   18;  Conservative    5;  Mismatches  10;  Indels   1;  Gaps   1;

Db    138 CQPCLDCGALHRHTRLLCS-RRDTDCGTCLPGFY 170
          | |||||: ::|  :  ||   |: || ||||||
Qy     89 CKPCLDCAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT    4
ID   NGFR_CHICK     STANDARD;      PRT;   416 AA.
AC   P18519;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE   (GP80-LNGFR) (P75 ICD).
GN   NGFR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC   Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE; 90166579.
RA   LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
RA   SHOOTER E.M., REICHARDT L.F.;
RT   "Structure and developmental expression of the nerve growth factor
RT   receptor in the chicken central nervous system.";
RL   Neuron 2:1123-1134(1989).
RN   [2]
RP   SEQUENCE OF 21-416 FROM N.A.
RX   MEDLINE; 90152240.
RA   HEUER J.G., FATEMIE-NAINIE S., WHEELER E.F., BOTHWELL M.;
RT   "Structure and developmental expression of the chicken NGF receptor.";
RL   Dev. Biol. 137:287-304(1990).
CC   -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
CC       NT-3, AND NT-4.
CC   -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
CC       BOND FORMATION.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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CC   -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR   PIR; JN0006; JN0006.
DR   PIR; A60504; A60504.
DR   HSSP; P07174; 1NGR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 4.
DR   PFAM; PF00531; death; 1.
KW   Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW   Phosphorylation; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    416       LOW-AFFINITY NERVE GROWTH FACTOR
FT                                 RECEPTOR.
FT   DOMAIN       29    239       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    240    261       POTENTIAL.
FT   DOMAIN      262    416       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       23    181       4 X TNFR-CYS.
FT   REPEAT       23     57       TNFR-CYS 1.
FT   REPEAT       58    100       TNFR-CYS 2.
FT   REPEAT      101    140       TNFR-CYS 3.
FT   REPEAT      141    181       TNFR-CYS 4.
FT   DOMAIN      188    236       SER/THR-RICH.
FT   DOMAIN      333    410       DEATH DOMAIN.
FT   DISULFID     24     35       BY SIMILARITY.
FT   DISULFID     36     49       BY SIMILARITY.
FT   DISULFID     39     56       BY SIMILARITY.
FT   DISULFID     59     75       BY SIMILARITY.
FT   DISULFID     78     91       BY SIMILARITY.
FT   DISULFID     81     99       BY SIMILARITY.
FT   DISULFID    101    114       BY SIMILARITY.
FT   DISULFID    117    130       BY SIMILARITY.
FT   DISULFID    120    138       BY SIMILARITY.
FT   DISULFID    141    156       BY SIMILARITY.
FT   DISULFID    159    172       BY SIMILARITY.
FT   DISULFID    162    180       BY SIMILARITY.
FT   CARBOHYD     52     52       POTENTIAL.
FT   CONFLICT     36     36       C -> Y (IN REF. 2).
FT   CONFLICT    173    173       T -> K (IN REF. 2).
FT   CONFLICT    276    276       N -> S (IN REF. 2).
FT   CONFLICT    396    396       K -> R (IN REF. 2).
SQ   SEQUENCE   416 AA;  44654 MW;  4D3F086A CRC32;

  Query Match           4.7%;  Score 146;  DB 1;  Length 416;
  Best Local Similarity  30.0%;  Pred. No. 1.08e-09;
  Matches   54;  Conservative   29;  Mismatches  83;  Indels  14;  Gaps  13;

Db     90 PC-VESDDAVCRCAYGYFQDELSGSCKECSICEVGFGLMFPCR-D-SQDTVCEECPEGTF 146
          :| |  : : ||     |:|  ||:|  |: |  |  |   |    ::|: |  |    |
Qy     24 SCKVTCESGDCR-QQE-FRDR-SGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRF 80

Db    147 SDEANFVDPCLPCTICEENEVMVK-ECTATSDAECRDLHPRWTTHTPSLAGSDSPEPITR 205
           ::  | : | ||  |   :   | :|:||||| | |  |     |  | | :  | :
Qy     81 KEDWGF-QKCKPCLDCAVVNRFQKANCSATSDAICGDCLPGFYRKT-KLVGFQDMECVPC 138

Db    206 DPFNTEGMATTLADIVTTVMGSSQPVVSRGTADNLIPVYCSILAAVVVGL-VAYIAF-KR 263
                  |  |  |: :| :  :| ||  | :| || ||:|:::| :  : : ||
Qy    139 GD-PPPPYEPHCASKVNLVKIASTASSPRDTA--LAAVICSALATVLLALLILCVIYCKR 195


RESULT    5
ID   TNR1_PIG       STANDARD;      PRT;   461 AA.
AC   P50555;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFRSF1A OR TNFR1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 96011645.
RA   SUTER B., PAULI U.H.;
RT   "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
RT   receptor.";
RL   Gene 163:263-266(1995).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19994; AAC48499.1; -.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 3.
DR   PFAM; PF00531; death; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN       22    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    233       POTENTIAL.
FT   DOMAIN      234    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    195       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    195       TNFR-CYS 4.
FT   DOMAIN      340    350       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      362    447       DEATH DOMAIN.
FT   DISULFID     44     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     81       BY SIMILARITY.
FT   DISULFID     84     99       BY SIMILARITY.
FT   DISULFID    102    117       BY SIMILARITY.
FT   DISULFID    105    125       BY SIMILARITY.
FT   DISULFID    127    143       BY SIMILARITY.
FT   DISULFID    146    158       BY SIMILARITY.
FT   DISULFID    149    166       BY SIMILARITY.
FT   DISULFID    168    179       BY SIMILARITY.
FT   DISULFID    182    190       BY SIMILARITY.
FT   DISULFID    185    194       BY SIMILARITY.
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD     86     86       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
SQ   SEQUENCE   461 AA;  50696 MW;  8E2C350A CRC32;

  Query Match           4.7%;  Score 146;  DB 1;  Length 461;
  Best Local Similarity  25.5%;  Pred. No. 1.08e-09;
  Matches   28;  Conservative   22;  Mismatches  55;  Indels   5;  Gaps   5;
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Db     44 CPQGKYSHPQNRSICCTKCHKGTYLHNDC-LGPGLDTDCRECDNGTFTASENHLTQCLSC 102
          | |  :       : |  |  |  | ::| :| | |::|  |    |   :  :  | :|
Qy     34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPC 92

Db    103 SKCRSEMSQVEISPCTVDRDTVCG-CRKNQYRKYWSETLFQCLNCSLCPN 151
            | : ::: : : |:   |::|| |    |||      || ::|  | :
Qy     93 LDC-AVVNRFQKANCSATSDAICGDCLPGFYRKT-KLVGFQDMECVPCGD 140


RESULT    6
ID   TNR1_MOUSE     STANDARD;      PRT;   454 AA.
AC   P25118;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91187885.
RA   LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RA   WONG G.H., CHEN E.Y., GOEDDEL D.V.;
RT   "Cloning and expression of cDNAs for two distinct murine tumor
RT   necrosis factor receptors demonstrate one receptor is species
RT   specific.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91246168.
RA   GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA   COPELAND N.G., JENKINS N.A., SMITH C.A.;
RT   "Molecular cloning and expression of the type 1 and type 2 murine
RT   receptors for tumor necrosis factor.";
RL   Mol. Cell. Biol. 11:3020-3026(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91285014.
RA   BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONERGHIS A.M.,
RA   GRAY P.W., FELDMANN M., FOXWELL B.M.J.;
RT   "Cloning, expression and cross-linking analysis of the murine p55
RT   tumor necrosis factor receptor.";
RL   Eur. J. Immunol. 21:1649-1656(1991).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE; 92039815.
RA   ROTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.;
RT   "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL   Immunogenetics 34:338-340(1991).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94245292.
RA   BEBO B.F., LINTHICUM D.S.;
RT   "Nucleotide sequence of the TNF type I receptor from a mouse
RT   endothelioma cell line.";
RL   Immunogenetics 39:450-451(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93156721.
RA   ROTHE J., BLUETHMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.;
RT   "Genomic organization and promoter function of the murine tumor
RT   necrosis factor receptor beta gene.";
RL   Mol. Immunol. 30:165-175(1993).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M60468; AAA39751.1; -.
DR   EMBL; M59377; AAA40464.1; -.
DR   EMBL; X59238; CAA41922.1; -.
DR   EMBL; X57796; CAA40936.1; -.
DR   EMBL; L26349; AAA59361.1; -.
DR   EMBL; M76656; AAA40465.1; -.
DR   EMBL; M88067; AAA40465.1; JOINED.
DR   EMBL; M76655; AAA40465.1; JOINED.
DR   PIR; A38634; GQMST1.
DR   PIR; S16677; S16677.
DR   PIR; S19021; S19021.
DR   HSSP; P19438; 1EXT.
DR   MGD; MGI:1314884; TNFRSF1A.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 4.
DR   PFAM; PF00531; death; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL       1    21       POTENTIAL.
FT   CHAIN       22   454       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22   212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   213   235       POTENTIAL.
FT   DOMAIN     236   454       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43   196       4 X TNFR-CYS.
FT   REPEAT      43    82       TNFR-CYS 1.
FT   REPEAT      83   125       TNFR-CYS 2.
FT   REPEAT     126   166       TNFR-CYS 3.
FT   REPEAT     167   196       TNFR-CYS 4.
FT   DOMAIN     339   349       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     356   441       DEATH DOMAIN.
FT   DISULFID    44    58       BY SIMILARITY.
FT   DISULFID    59    72       BY SIMILARITY.
FT   DISULFID    62    81       BY SIMILARITY.
FT   DISULFID    84    99       BY SIMILARITY.
FT   DISULFID   102   117       BY SIMILARITY.
FT   DISULFID   105   125       BY SIMILARITY.
FT   DISULFID   127   143       BY SIMILARITY.
FT   DISULFID   146   158       BY SIMILARITY.
FT   DISULFID   149   166       BY SIMILARITY.
FT   DISULFID   168   179       BY SIMILARITY.
FT   DISULFID   182   191       BY SIMILARITY.
FT   DISULFID   185   195       BY SIMILARITY.
FT   CARBOHYD    54    54       POTENTIAL.
FT   CARBOHYD   151   151       POTENTIAL.
FT   CARBOHYD   202   202       POTENTIAL.
FT   CONFLICT   394   394       R -> G (IN REF. 6).
SQ   SEQUENCE   454 AA;  50129 MW;  4B6EEC09 CRC32;

  Query Match             4.6%;  Score 142;  DB 1;  Length 454;
  Best Local Similarity  26.9%;  Pred. No. 6.22e-09;
  Matches    29;  Conservative   16;  Mismatches  58;  Indels   5;  Gaps   5;

Db     44 CPQGKYVHSXNNSICCTKCHKGTYLVSDCPSP-GRDTVCRECEKGTFTASQNYLRQCLSC 102
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          | |  :     | : |  |  |  |  :|    | |: |  |    |     : : | :|
Qy      34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGFQK-CKPC 92

Db     103 KTCRKEMSQVEISPCQADKDTVCG-CKENQFQRYLSETHFQCVDCSPC 149
           |   ::: : : | |  |::|| |    | |      || ::| ||
Qy      93 LDCA-VVNRFQKANCSATSDAICGDCLPG-FYRKTKLVGFQDMECVPC 138


RESULT    7
ID   TNR1_HUMAN     STANDARD;      PRT;   455 AA.
AC   P19438;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR
DE   BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (P55) (CD120A).
GN   TNFRSF1A OR TNFR1 OR TNFAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 90235285.
RA   SCHALL T.J., LEWIS M., KOLLER K.J., LEE A., RICE G.C., WONG G.H.W.,
RA   GETANAGA T., GRANGER G.A., LENTZ R., RAAB H., KOHR W.J., GOEDDEL D.V.;
RT   "Molecular cloning and expression of a receptor for human tumor
RT   necrosis factor.";
RL   Cell 61:361-370(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 90235284.
RA   LOETSCHER H., PAN Y.-C.E., LAHM H.-W., GENTZ R., BROCKHAUS M.,
RA   TABUCHI H., LESSLAUER W.;
RT   "Molecular cloning and expression of the human 55 kd tumor necrosis
RT   factor receptor.";
RL   Cell 61:351-359(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX   MEDLINE; 91006021.
RA   NOPHAR Y., KEMPER O., BRAKEBUSCH C., ENGELMANN H., ZWANG R.,
RA   ADERKA D., HOLTMANN H., WALLACH D.;
RT   "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
RT   for the type I TNF-R, cloned using amino acid sequence data of its
RT   soluble form, encodes both the cell surface and a soluble form of the
RT   receptor.";
RL   EMBO J. 9:3269-3278(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 91017509.
RA   GRAY P.W., BARRETT K., CHANTRY D., TURNER M., FELDMAN M.;
RT   "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
RT   expression of recombinant soluble TNF-binding protein.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92250049.
RA   FUCHS P., STREHL S., DWORZAK M., HIMMLER A., AMBROS P.F.;
RT   "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
RT   localization to chromosome 12p13.";
RL   Genomics 13:219-224(1992).
RN   [7]
RP   SEQUENCE OF 41-45.
RX   MEDLINE; 90110215.
RA   ENGELMANN H., NOVICK D., WALLACH D.;
RT   "Two tumor necrosis factor-binding proteins purified from human
RT   urine. Evidence for immunological cross-reactivity with cell surface
RT   tumor necrosis factor receptors.";
RL   J. Biol. Chem. 265:1531-1536(1990).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
RX   MEDLINE; 93258809.
RA   BANNER D.W., D'ARCY A., JANES W., GENTZ R., SCHOENFELD H.-J.,
RA   BROGER C., LOETSCHER H., LESSLAUER W.;
RT   "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT   beta complex: implications for TNF receptor activation.";
RL   Cell 73:431-445(1993).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX   MEDLINE; 97094982.
RA   NAISMITH J.H., DEVINE T.Q., KHONO H., SPRANG S.R.;
RT   "Structures of the extracellular domain of the type I tumor necrosis
RT   factor receptor.";
RL   Structure 4:1251-1262(1996).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
CC       NONCYTOCIDAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
CC       OF THE ACID SPLINGOMIYELINASE.
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
CC       THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
CC       NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X55313; CAA39021.1; -.
DR   EMBL; M33294; AAA03210.1; -.
DR   EMBL; M58286; AAA36753.1; -.
DR   EMBL; M63121; AAA36754.1; -.
DR   EMBL; M75866; AAA61201.1; -.
DR   EMBL; M75864; AAA61201.1; JOINED.
DR   EMBL; M75865; AAA61201.1; JOINED.
DR   EMBL; M60275; AAA36756.1; -.
DR   EMBL; A21522; CAA01558.1; -.
DR   PIR; A34899; GQHUT1.
DR   PIR; A35010; A35010.
DR   PIR; S12057; S12057.
DR   PIR; A38208; A38208.
DR   PDB; 1TNR; 31-JUL-94.
DR   PDB; 1NCF; 07-DEC-95.
DR   PDB; 1EXT; 11-JAN-97.
DR   MIM; 191190; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
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DR   PFAM; PF00020; TNFR_c6; 4.
DR   PFAM; PF00531; death; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
KW   3D-structure.
FT   SIGNAL        1     21
FT   CHAIN        22    455       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   CHAIN        41    291       TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT   DOMAIN       22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    234       POTENTIAL.
FT   DOMAIN      235    455       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       43    196       4 X TNFR-CYS.
FT   REPEAT       43     82       TNFR-CYS 1.
FT   REPEAT       83    125       TNFR-CYS 2.
FT   REPEAT      126    166       TNFR-CYS 3.
FT   REPEAT      167    196       TNFR-CYS 4.
FT   DOMAIN      338    348       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN      356    441       DEATH DOMAIN.
FT   DISULFID     44     58
FT   DISULFID     59     72
FT   DISULFID     62     81
FT   DISULFID     84     99
FT   DISULFID    102    117
FT   DISULFID    105    125
FT   DISULFID    127    143
FT   DISULFID    146    158
FT   DISULFID    149    166
FT   DISULFID    168    179
FT   DISULFID    182    191
FT   DISULFID    185    195
FT   CARBOHYD     54     54       POTENTIAL.
FT   CARBOHYD    145    145       POTENTIAL.
FT   CARBOHYD    151    151       POTENTIAL.
FT   CONFLICT    412    412       MISSING (IN REF. 4).
FT   CONFLICT    443    446       GPAA -> APP (IN REF. 4).
SQ   SEQUENCE   455 AA;  50494 MW;  CE0EA06F CRC32;

  Query Match             4.6%;  Score 143;  DB 1;  Length 455;
  Best Local Similarity  25.2%;  Pred. No. 4.02e-09;
  Matches    32;  Conservative   30;  Mismatches  57;  Indels   8;  Gaps   8;

Db     11 LPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV-CPQGKYIHPQNNSICCTKCHKGTYL 68
          ::| ||||    :: : :: |:  |: :   :|  | |  :     | : |  |  |  |
Qy      1 MALKVLLEQEKTFF-TLLV-LLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMEL 58

Db     69 YNDCP-GPGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCG- 126
           ::|  | |:|::|  |    |   :  :: | :|  |   : : : ::|:   |::||
Qy     59 SKECGFGYGEDAQCVACRLHRFKE-DWGFQKCKPCLDCA-VVNRFQKANCSATSDAICGD 116

Db    127 CRKNQYR 133
          |    ||
Qy    117 CLPGFYR 123


RESULT    8
ID   TNRC_HUMAN     STANDARD;      PRT;   435 AA.
AC   P36941;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE   2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN   LTBR OR TNFCR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LIVER;
RX   MEDLINE; 93252381.
RA   BAENS M., CHAFFANET M., CASSIMAN J.J., DEN BERGHE H., MARYNEN P.;
RT   "Construction and evaluation of a hncDNA library of human 12p
RT   transcribed sequences derived from a somatic cell hybrid.";
RL   Genomics 16:214-218(1993).
RN   [2]
RP   FUNCTION.
RX   MEDLINE; 94225209.
RA   CROWE P.D., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSION C.,
RA   EHRENFELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.;
RT   "A lymphotoxin-beta-specific receptor.";
RL   Science 264:707-710(1994).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L04270; AAA36757.1; -.
DR   HSSP; P25942; 1CDF.
DR   MIM; 600979; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PFAM; PF00020; TNFR_c6; 4.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    435       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN       31    227       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    228    248       POTENTIAL.
FT   DOMAIN      249    435       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       42    211       4 X TNFR-CYS.
FT   REPEAT       42     81       TNFR-CYS 1.
FT   REPEAT       82    124       TNFR-CYS 2.
FT   REPEAT      125    168       TNFR-CYS 3.
FT   REPEAT      169    211       TNFR-CYS 4.
FT   DISULFID     43     58       BY SIMILARITY.
FT   DISULFID     59     72       BY SIMILARITY.
FT   DISULFID     62     80       BY SIMILARITY.
FT   DISULFID     83     98       BY SIMILARITY.
FT   DISULFID    101    116       BY SIMILARITY.
FT   DISULFID    104    124       BY SIMILARITY.
FT   DISULFID    126    132       BY SIMILARITY.
FT   DISULFID    139    148       BY SIMILARITY.
FT   DISULFID    142    167       BY SIMILARITY.
FT   DISULFID    170    185       BY SIMILARITY.
FT   CARBOHYD     40     40       POTENTIAL.
FT   CARBOHYD    177    177       POTENTIAL.
SQ   SEQUENCE   435 AA;  46709 MW;  203B82DD CRC32;

  Query Match             4.4%;  Score 136;  DB 1;  Length 435;
  Best Local Similarity  26.3%;  Pred. No. 8.24e-08;
  Matches    26;  Conservative   24;  Mismatches  41;  Indels   8;  Gaps   8;

Db     37 ASENQTCRDQEKEYYE-PQHRICCSRCPPGTYVSAKCS-RI-RDTVCATCAENSYNEHWN 93
          : |:  || |: |: : : : : |::| ||  :|  |:     |: | :|  : ::| |
Qy     28 TCESGDCR-QQ-EFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG 85

Db     94 YLTICQLCRPCDPVMGLEEIAPCTSKRKTQC-RCQPGMF 131
          :   |  |  |  |  ::  | |::   : |  | || :
Qy     86 FQK-CKPCLDCAVVNRFQK-ANCSATSDAICGDCLPGFY 122


RESULT    9
ID   FASA_HUMAN     STANDARD;      PRT;   335 AA.
AC   P25445;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE   (APO-1 ANTIGEN) (CD95 ANTIGEN).
GN   APT1 OR FAS.
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91309137.
RA   ITOH N., YONEHARA S., ISHII A., YONEHARA M., MIZUSHIMA S.I.,
RA   SAMESHIMA M., HASE A., SETO Y., NAGATA S.;
RT   "The polypeptide encoded by the cDNA for human cell surface antigen
RT   Fas can mediate apoptosis.";
RL   Cell 66:233-243(1991).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX   MEDLINE; 92268122.
RA   OEHM A., BEHRMANN I., FALK W., PAWLITA M., MAIER G., KLAS C.,
RA   LI-WEBER M., RICHARDS S., DHEIN J., TRAUTH B.C., PONSTINGL H.,
RA   KRAMMER P.H.;
RT   "Purification and molecular cloning of the APO-1 cell surface
RT   antigen, a member of the tumor necrosis factor/nerve growth factor
RT   receptor superfamily. Sequence identity with the Fas antigen.";
RL   J. Biol. Chem. 267:10709-10715(1992).
RN   [3]
RP   STRUCTURE BY NMR OF 218-335.
RX   MEDLINE; 97122332.
RA   HUANG B., EBERSTADT M., OLEJNICZAK E.T., MEADOWS R.P., FESIK S.W.;
RT   "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL   Nature 384:638-641(1996).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC       ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC       RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC       SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC       ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC       CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC       APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC       INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC       SUICIDE OF MATURE T-CELLS, OR BOTH.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M67454; AAA63174.1; -.
DR   EMBL; X63717; CAA45250.1; -.
DR   PIR; A40036; A40036.
DR   PIR; S24543; S24543.
DR   PDB; 1DDF; 12-NOV-97.
DR   MIM; 134637; -.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 2.
DR   PFAM; PF00531; death; 1.
KW   Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW   3D-structure.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    335       FASL RECEPTOR.
FT   DOMAIN       17    173       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    174    190       POTENTIAL.
FT   DOMAIN      191    335       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       47    166       3 X TNFR-CYS.
FT   REPEAT       47     83       TNFR-CYS 1.
FT   REPEAT       84    127       TNFR-CYS 2.
FT   REPEAT      128    166       TNFR-CYS 3.
FT   DOMAIN      230    314       DEATH DOMAIN.
FT   CARBOHYD    118    118       POTENTIAL.
FT   CARBOHYD    136    136       POTENTIAL.
SQ   SEQUENCE   335 AA;  37732 MW;  3BF8F973 CRC32;

  Query Match             4.3%;  Score 133;  DB 1;  Length 335;
  Best Local Similarity  26.9%;  Pred. No. 2.94e-07;
  Matches    21;  Conservative   21;  Mismatches  30;  Indels   6;  Gaps   6;

Db      59 CHKPCPPGERKARDCTVN-GDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEI 117
           |:  | ||   :::|    |::::||:|:  : : :   |  ||: |  |   : ::
Qy      49 CNQ-CGPGMELSKECGFGYGEDAQCVACRLHR-FKEDWGFQ-KCKPCLDCAVVNRFQ-KA 104

Db     118 NCTRTQNTKC-RCKPNFF 134
           ||: | :: |  | | |:
Qy     105 NCSATSDAICGDCLPGFY 122


RESULT   10
ID   VT2_MYXVL      STANDARD;      PRT;   326 AA.
AC   P29825;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN   T2.
OS   Myxoma virus (strain Lausanne).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Leporipoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91335768.
RA   UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
RT   "Myxoma virus expresses a secreted protein with homology to the tumor
RT   necrosis factor receptor gene family that contributes to viral
RT   virulence.";
RL   Virology 184:370-382(1991).
CC   -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC       REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC       ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M95181; AAA46632.1; -.
DR   EMBL; A23729; CAA01688.1; -.
DR   PIR; A40566; GQVZML.
DR   HSSP; P19438; 1TNR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
KW   Receptor; Glycoprotein; Repeat; Signal.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    326       TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT   DOMAIN       27    186       4 X TNFR-CYS.
FT   REPEAT       27     62       TNFR-CYS 1.
FT   REPEAT       63    104       TNFR-CYS 2.
FT   REPEAT      105    147       TNFR-CYS 3.
FT   REPEAT      148    186       TNFR-CYS 4.
FT   CARBOHYD     66     66       POTENTIAL.
FT   CARBOHYD    181    181       POTENTIAL.
FT   CARBOHYD    205    205       POTENTIAL.
FT   CARBOHYD    238    238       POTENTIAL.
SQ   SEQUENCE   326 AA;  35208 MW;  2F059A61 CRC32;

  Query Match             4.2%;  Score 130;  DB 1;  Length 326;
  Best Local Similarity  29.5%;  Pred. No. 1.03e-06;
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  Matches    28;  Conservative   16;  Mismatches  42;  Indels   9;  Gaps   8;

Db      24 DRGKCRGNDY-EKDGLC--CTSCPPGSYASRLCG-P-GSDTVCSPCKNETFTASTNHAPA 78
           : | ||  :: :: | |  |  | ||   |: ||   | |: | :|:   |
Qy      30 ESGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGF-QK 88

Db      79 CVSCRGRCTG-HLSESQSCDKTRDRVC-DCSAGNY 111
           | :|   |:  :  :  :|  | | :| || :| |
Qy      89 CKPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   11
ID   TNRC_MOUSE     STANDARD;      PRT;   415 AA.
AC   P50284;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN   LTBR OR TNFCR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CVB; TISSUE=LUNG;
RX   MEDLINE; 96072804.
RA   FORCE W.R., WALTER B.N., HESSION C., TIZARD R., KOZAK C.A.,
RA   BROWNING J.L., WARE C.F.;
RT   "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT   and expression.";
RL   J. Immunol. 155:5280-5288(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 96163885.
RA   NAKAMURA T., TASHIRO K., NAZAREA M., NAKANO T., SASAYAMA S.,
RA   HONJO T.;
RT   "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT   sequence trap and chromosomal mapping.";
RL   Genomics 30:312-319(1995).
CC   -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC       IMMUNE DEVELOPMENT.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U29173; AAA68964.1; -.
DR   EMBL; L38423; AAB00846.1; -.
DR   EMBL; U30798; AAA81334.1; -.
DR   HSSP; P25942; 1CDF.
DR   MGD; MGI:104875; LTBR.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PFAM; PF00020; TNFR_c6; 3.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT   SIGNAL       1     30       POTENTIAL.
FT   CHAIN       31    415       LYMPHOTOXIN-BETA RECEPTOR.
FT   DOMAIN      31    223       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   224    244       POTENTIAL.
FT   DOMAIN     245    415       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      42    213       4 X TNFR-CYS.
FT   REPEAT      42     81       TNFR-CYS 1.
FT   REPEAT      82    124       TNFR-CYS 2.
FT   REPEAT     125    170       TNFR-CYS 3.
FT   REPEAT     171    213       TNFR-CYS 4.
FT   DISULFID    43     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     80       BY SIMILARITY.
FT   DISULFID    83     98       BY SIMILARITY.
FT   DISULFID   101    116       BY SIMILARITY.
FT   DISULFID   104    124       BY SIMILARITY.
FT   DISULFID   126    132       BY SIMILARITY.
FT   DISULFID   139    150       BY SIMILARITY.
FT   DISULFID   142    169       BY SIMILARITY.
FT   DISULFID   172    187       BY SIMILARITY.
FT   CARBOHYD    40     40       POTENTIAL.
FT   CARBOHYD   179    179       POTENTIAL.
SQ   SEQUENCE   415 AA;  44956 MW;  3C5DD121 CRC32;

  Query Match          4.2%;  Score 130;  DB 1;  Length 415;
  Best Local Similarity  30.3%;  Pred. No. 1.03e-06;
  Matches    23;  Conservative   16;  Mismatches  32;  Indels   5;  Gaps   5;

Db      57 VCCSRCPPGEFVFAVCS-R-SQDTVCKTCPHNSYNEHWNHLSTCQLCRPCDIVLGFEEVA 114
           | |:::| ||  :   |:   ::|: | :|  : ::| |  :  |  |  | :|  |:  |
Qy      47 VPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWG-FQKCKPCLDCAVVNRFQK-A 104

Db     115 PCTSDRKAEC-RCQPG 129
           |::   | |  | ||
Qy     105 NCSATSDAICGDCLPG 120


RESULT   12
ID   TNR1_RAT       STANDARD;      PRT;   461 AA.
AC   P22934;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN   TNFRSF1A OR TNFR1 OR TNFR-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 91090841.
RA   HIMMLER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFIZENMAIER K.,
RA   LANTZ M., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;
RT   "Molecular cloning and expression of human and rat tumor necrosis
RT   factor receptor chain (p60) and its soluble derivative, tumor
RT   necrosis factor-binding protein.";
RL   DNA Cell Biol. 9:705-715(1990).
CC   -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC       RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC       AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC       PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC       SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC       PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC   -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC       HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC       PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC       WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC       PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC       TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC       ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC       NF-KAPPA B SIGNALING (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63122; AAA42256.1; -.
DR   PIR; B36555; B36555.
DR   HSSP; P19438; 1TNR.
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DR   PROSITE; PS00652; TNFR_NGFR_1; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 4.
DR   PFAM; PF00531; death; 1.
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    461       TUMOR NECROSIS FACTOR RECEPTOR 1.
FT   DOMAIN      22    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   212    234       POTENTIAL.
FT   DOMAIN     235    461       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43    196       4 X TNFR-CYS.
FT   REPEAT      43     82       TNFR-CYS 1.
FT   REPEAT      83    125       TNFR-CYS 2.
FT   REPEAT     126    166       TNFR-CYS 3.
FT   REPEAT     167    196       TNFR-CYS 4.
FT   DOMAIN     344    354       N-SMASE ACTIVATION DOMAIN (NSD).
FT   DOMAIN     363    448       DEATH DOMAIN.
FT   DISULFID    44     58       BY SIMILARITY.
FT   DISULFID    59     72       BY SIMILARITY.
FT   DISULFID    62     81       BY SIMILARITY.
FT   DISULFID    84     99       BY SIMILARITY.
FT   DISULFID   102    117       BY SIMILARITY.
FT   DISULFID   105    125       BY SIMILARITY.
FT   DISULFID   127    143       BY SIMILARITY.
FT   DISULFID   146    158       BY SIMILARITY.
FT   DISULFID   149    166       BY SIMILARITY.
FT   DISULFID   168    179       BY SIMILARITY.
FT   DISULFID   182    191       BY SIMILARITY.
FT   DISULFID   185    195       BY SIMILARITY.
FT   CARBOHYD    54     54       POTENTIAL.
FT   CARBOHYD   151    151       POTENTIAL.
FT   CARBOHYD   201    201       POTENTIAL.
SQ   SEQUENCE   461 AA;  50969 MW;  82F68B08 CRC32;

  Query Match           4.2%;  Score 130;  DB 1;  Length 461;
  Best Local Similarity  25.9%;  Pred. No. 1.03e-06;
  Matches   28;  Conservative   16;  Mismatches  59;  Indels   5;  Gaps   5;

Db     44 CPQGKYAHPKNNSICCTKCHKGTYLVSDCPSP-GQETVCEVCDKGTFTASQNHVRQCLSC 102
          | |  :     | : |  |  |  |  :|    |::: |  |    |       : | :|
Qy     34 CRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKEDWGF-QKCKPC 92

Db    103 KTCRKEMFQVEISPCKADMDTVCG-CKKNQFQRYLSETHFQCVDCSPC 149
            |   : : : : | |  |::|| |    | |      || ::| ||
Qy     93 LDCA-VVNRFQKANCSATSDAICGDCLPG-FYRKTKLVGFQDMECVPC 138


RESULT   13
ID   FASA_MOUSE     STANDARD;      PRT;   327 AA.
AC   P25446;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE   (APO-1 ANTIGEN) (CD95).
GN   APT1 OR FAS.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 92148151.
RA   WATANABE-FUKUNAGA R., BRANNAN C.I., ITOH N., YONEHARA S.,
RA   COPELAND N.G., JENKINS N.A., NAGATA S.;
RT   "The cDNA structure, expression, and chromosomal assignment of the
RT   mouse Fas antigen.";
RL   J. Immunol. 148:1274-1279(1992).
RN   [2]
RP   SEQUENCE OF 1-96 FROM N.A.
RX   MEDLINE; 93189576.
RA   ADACHI M., WATANABE-FUKUNAGA R., NAGATA S.;
RT   "Aberrant transcription caused by the insertion of an early
RT   transposable element in an intron of the Fas antigen gene of lpr
RT   mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN   [3]
RP   VARIANT LPR.
RX   MEDLINE; 92195401.
RA   WATANABE-FUKUNAGA R., BRANNAN C.I., COPELAND N.G., JENKINS N.A.,
RA   NAGATA S.;
RT   "Lymphoproliferation disorder in mice explained by defects in Fas
RT   antigen that mediates apoptosis.";
RL   Nature 356:314-317(1992).
CC   -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC       ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC       RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC       SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC       ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC       CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC       APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC       INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC       SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC       LIVER, LUNG, HEART, AND ADULT OVARY.
CC   -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC       AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC   -!- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC       DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC       PRODUCTION.
CC   -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M83649; AAA37593.1; -.
DR   EMBL; S56490; AAB25700.1; -.
DR   EMBL; S56485; AAB25700.1; JOINED.
DR   EMBL; S56486; AAB25700.1; JOINED.
DR   PIR; A46484; A46484.
DR   HSSP; P25445; 1DDF.
DR   MGD; MGI:95484; FAS.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PFAM; PF00020; TNFR_c6; 3.
DR   PFAM; PF00531; death; 1.
KW   Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW   Disease mutation.
FT   SIGNAL       1     21
FT   CHAIN       22    327       FASL RECEPTOR.
FT   DOMAIN      22    169       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   170    186       POTENTIAL.
FT   DOMAIN     187    327       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      43    162       3 X TNFR-CYS.
FT   REPEAT      43     79       TNFR-CYS 1.
FT   REPEAT      80    123       TNFR-CYS 2.
FT   REPEAT     124    162       TNFR-CYS 3.
FT   DOMAIN     222    306       DEATH DOMAIN.
FT   CARBOHYD    43     43       POTENTIAL.
FT   CARBOHYD   114    114       POTENTIAL.
FT   VARIANT    246    246       I -> N (IN LPR).
SQ   SEQUENCE   327 AA;  37418 MW;  22D6DC39 CRC32;

  Query Match           4.1%;  Score 127;  DB 1;  Length 327;
  Best Local Similarity  26.0%;  Pred. No. 3.58e-06;
  Matches   20;  Conservative   18;  Mismatches  34;  Indels   5;  Gaps   5;

Db     56 CQPCQPGKKKVEDCKMN-GGTPTCAPCTEGKEYMDKNHYADKCRRCTLCDEEHGLEVETN 114
          | | ||:    :|    |  : | :|   : :::   : :||: |  |   : ::  :|
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Qy     49 CNQCGPGMELSKECGFGYGEDAQCVACRLHR-FKEDWGF-QKCKPCLDCAVVNRFQ-KAN 105

Db    115 CTLTQNTKC-KCKPDFY 130
          |: | :: |  | | ||
Qy    106 CSATSDAICGDCLPGFY 122


RESULT   14
ID   VC22_VARV      STANDARD;      PRT;   349 AA.
AC   P34015;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   PROTEIN C22/B28 HOMOLOG.
GN   G4R.
OS   Variola virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=INDIA-1967 / ISOLATE IND3;
RX   MEDLINE; 93202281.
RA   SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
RT   "Genes of variola and vaccinia viruses necessary to overcome the host
RT   protective mechanisms.";
RL   FEBS Lett. 319:80-83(1993).
CC   -!- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X69198; CAA49137.1; -.
DR   EMBL; X67117; CAA47540.1; -.
DR   PIR; D36858; D36858.
DR   PIR; S35987; S35987.
DR   PIR; S46888; S46888.
DR   HSSP; P19438; 1NCF.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
DR   PFAM; PF00020; TNFR_c6; 2.
KW   Repeat.
FT   DOMAIN       31    108       2 X TNFR-CYS.
FT   REPEAT       31     66       TNFR-CYS 1.
FT   REPEAT       67    108       TNFR-CYS 2.
SQ   SEQUENCE   349 AA;  38189 MW;  50D0B435 CRC32;

  Query Match             4.1%;  Score 128;  DB 1;  Length 349;
  Best Local Similarity  28.7%;  Pred. No. 2.37e-06;
  Matches    27;  Conservative   21;  Mismatches  37;  Indels   9;  Gaps   8;

Db     29 NGKCKDTEYK-RHNLC--CLSCPPGTYASRLCD-S-KTNTQCTPCGSGTFTSRNNHLPAC 83
          :| |:: |:: |   |  |  | ||   |: | :   ::|| :|    |   :  :  |
Qy     31 SGDCRQQEFRDRSGNCVPCNQCGPGMELSKECGFGYGEDAQCVACRLHRFKE-DWGFQKC 89

Db     84 LSCNGRCNS-NQVETRSCNTTHNRIC-ECSPGYY 115
          :|   |   |: :  :|::| : || :| ||:|
Qy     90 KPCLD-CAVVNRFQKANCSATSDAICGDCLPGFY 122


RESULT   15
ID   LMG2_MOUSE     STANDARD;      PRT;  1192 AA.
AC   Q61092;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   LAMININ GAMMA-2 CHAIN PRECURSOR (KALININ/NICEIN/EPILIGRIN 100 KD
DE   SUBUNIT).
GN   LAMC2 OR B2T.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB; TISSUE=LUNG;
RX   MEDLINE; 95188894.
RA   SUGIYAMA S., UTANI A., YAMADA S., KOZAK C.A., YAMADA Y.;
RT   "Cloning and expression of the mouse laminin gamma 2 (B2t) chain, a
RT   subunit of epithelial cell laminin.";
RL   Eur. J. Biochem. 228:120-128(1995).
CC   -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC       IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC       CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC       WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC   -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC       DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC       TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC       COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC       THE GAMMA-2 CHAIN IS A SUBUNIT OF LAMININ-5 (EPILIGRIN/KALININ/
CC       NICEIN).
CC   -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC       MEMBRANES (MAJOR COMPONENT).
CC   -!- TISSUE SPECIFICITY: EPITHELIAL CELLS OF MANY TISSUES, PARTICULARLY
CC       HIGH LEVELS IN TONGUE, HAIR FOLLICLES AND KIDNEY. BASEMENT
CC       MEMBRANES OF THE COLLECTING TUBULES OF KIDNEY AND PANCREAS.
CC   -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC       WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC   -!- DOMAIN: DOMAIN IV IS GLOBULAR.
CC   -!- SIMILARITY: CONTAINS 7.5 LAMININ EGF-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U43327; AAA85256.1; -.
DR   HSSP; P02468; 1TLE.
DR   MGD; MGI:99913; LAMC2.
DR   PROSITE; PS00022; EGF_1; 3.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS01248; LAMININ_TYPE_EGF; 5.
DR   PFAM; PF00052; laminin_B; 1.
DR   PFAM; PF00053; laminin_EGF; 5.
KW   Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW   Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22   1192       LAMININ GAMMA-2 CHAIN.
FT   DOMAIN       28    196       3.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT                                III B).
FT   DOMAIN       28     83       LAMININ EGF-LIKE 1.
FT   DOMAIN       84    130       LAMININ EGF-LIKE 2.
FT   DOMAIN      139    186       LAMININ EGF-LIKE 3.
FT   DOMAIN      187    196       LAMININ EGF-LIKE 4 (N-TERMINAL).
FT   DOMAIN      197    382       LAMININ DOMAIN IV.
FT   DOMAIN      383    603       4 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT                                III A).
FT   DOMAIN      383    416       LAMININ EGF-LIKE 4 (C-TERMINAL).
FT   DOMAIN      417    462       LAMININ EGF-LIKE 5.
FT   DOMAIN      463    517       LAMININ EGF-LIKE 6.
FT   DOMAIN      518    573       LAMININ EGF-LIKE 7.
FT   DOMAIN      574    603       LAMININ EGF-LIKE 8 (INCOMPLETE).
FT   DOMAIN      604   1192       DOMAIN II AND I.
FT   DOMAIN      613    711       COILED COIL (POTENTIAL).
FT   DOMAIN      760    787       COILED COIL (POTENTIAL).
FT   DOMAIN      947    997       COILED COIL (POTENTIAL).
FT   DOMAIN     1140   1179       COILED COIL (POTENTIAL).
FT   SITE        587    589       CELL ATTACHMENT SITE (POTENTIAL).
FT   DISULFID     84     96       BY SIMILARITY.
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FT   DISULFID     86    102       BY SIMILARITY.
FT   DISULFID    104    113       BY SIMILARITY.
FT   DISULFID    116    128       BY SIMILARITY.
FT   DISULFID    139    150       BY SIMILARITY.
FT   DISULFID    141    155       BY SIMILARITY.
FT   DISULFID    157    166       BY SIMILARITY.
FT   DISULFID    169    184       BY SIMILARITY.
FT   DISULFID    463    471       BY SIMILARITY.
FT   DISULFID    465    482       BY SIMILARITY.
FT   DISULFID    485    494       BY SIMILARITY.
FT   DISULFID    497    515       BY SIMILARITY.
FT   DISULFID    518    532       BY SIMILARITY.
FT   DISULFID    520    539       BY SIMILARITY.
FT   DISULFID    542    551       BY SIMILARITY.
FT   DISULFID    554    571       BY SIMILARITY.
FT   DISULFID    611    611       INTERCHAIN (PROBABLE).
FT   DISULFID    614    614       INTERCHAIN (PROBABLE).
FT   DISULFID   1183   1183       INTERCHAIN (WITH CHAIN BETA-3)
FT                                (PROBABLY).
FT   CARBOHYD     342    342       POTENTIAL.
FT   CARBOHYD     363    363       POTENTIAL.
FT   CARBOHYD     527    527       POTENTIAL.
FT   CARBOHYD     942    942       POTENTIAL.
FT   CARBOHYD    1033   1033       POTENTIAL.
SQ   SEQUENCE   1192 AA;  130287 MW;  76A7C102 CRC32;

  Query Match            4.1%;  Score 126;  DB 1;  Length 1192;
  Best Local Similarity  32.1%;  Pred. No. 5.39e-06;
  Matches    35;  Conservative   18;  Mismatches  43;  Indels  13;  Gaps  11;

Db    386 LLGYKGQFCQ-ECASG-YKRDSARLGAFGACVPCN-CQGEGACDPDTGDCYSGDENPDIE 442
          |||| :  |   | ||  :::  |    | ||||| | | |  :    :|  |  : | :
Qy     19 LLGYLS--CKVTCESGDCRQQEFR-DRSGNCVPCNQC-GPGM-ELSK-ECGFGYGE-DAQ 71

Db    443 CADCPIGFYNDPHDPRSCKPC-PCH--NGFSCSVMPETEEVVCNNCPPG 488
          |  | :  :::    : ||||  |   | |  :  : | : :| :| ||
Qy     72 CVACRLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG 120


Search completed: Tue Apr 18 14:00:34 2000
Job time : 43 secs.
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